

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4892:

CTCTTAACCT TGCAGCACCG GGCAGGCGTC AGCCCGTATA CATCACCTTA CGGTTTGACG 60
 AGACCGTGTG TTTTGTAGAA ACAGGTGC 88

(2) INFORMATION FOR SEQ ID NO: 4893:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4893:

TAGCGAATGA GATAAACGCG GCGGACTGTA AATCCGCTCC TTCGGGTTCC GCAGTTCGAA 60
 TCTGCCCCCC TCCATTATT ATTTTnAAAA AAAGCATAGT TC 102

(2) INFORMATION FOR SEQ ID NO: 4894:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4894:

CGAGCGATTG CGACTCAGAC AATGACTCGG AATTCAGATA ACGAATCTGA CTCAGACAGT 60
 GACTCAGATT CCGACAGT 78

(2) INFORMATION FOR SEQ ID NO: 4895:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4895:

TTAGTATTGG CACTCACATG TCACATGCTT CACTCGACCT ATTACCTCAC ACTTGGGGAC 120
 TTATACCGAG TnGGAATCTC A 141

5 (2) INFORMATION FOR SEQ ID NO: 4896:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4896:

15 GTTCGGATTT AATTGATTC ATTGTGCG TAAATTCAGA AGCCATTITA TGAAGAAGAGT 60
 GATTTAATTC ATAAATTCT 80

20 (2) INFORMATION FOR SEQ ID NO: 4897:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4897:

30 GGTATGGCTG GCGCTTTACG TGCCACATTA GATTATGTCA CTGAGCGTAA GAAGTTCGGC 60
 AAACCAATTA GTA 73

35 (2) INFORMATION FOR SEQ ID NO: 4898:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4898:

45 GTGCCGAGGA CCGGAATCGA ACCGGTACGG TGATCACTCA CCGCAGGATT TTAAGTCCTG 60
 TCGCTCTGCC A 71

(2) INFORMATION FOR SEQ ID NO: 4899:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4899:

AGCGCTGGA TTCCACGGTG TAAGCAGTAA GGCTGAGTAT TAGGCAAATC CGGTACTCGT 60

TAAGGCTGGA GCTGTnGATG GGGAGAAGAC ATGTGTGCTT ACGTAGTGCG TGGTTT 116

(2) INFORMATION FOR SEQ ID NO: 4900:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4900:

TTCCGGCCCC TGGCGGnTC CTAGGAGTTC CACGGAACCC CAGGATTTTG TAGGACCCCC 60

CGGGCAGAGT CCCCTTCGAC TAAGAAAAATC TCACATTCTT CAGGACTTTT TAC 113

(2) INFORMATION FOR SEQ ID NO: 4901:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4901:

ACTTAATGGA TTGATTAAGT AGTGGGTCTT TAACATTAGG CCTCAGCTAA TGTGCTACTT 60

AAAAATAGGG AATACATG 78

(2) INFORMATION FOR SEQ ID NO: 4902:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4902:

ATGGGACATG GTGTGCCTCC TTGCTATAGT CACCAGACAT ATGAATGTAA TTTATACATT 60

CAAAACTAGA TAGTAAGTAA AAGT 84

(2) INFORMATION FOR SEQ ID NO: 4903:

(A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4903:

10 TTGTCGGGTA AGTTCGACC CGCACGAAAG GCGTAACGAT TTTGGCACTG TCTCAACGAG 60
 AGACTCGGTG 70

(2) INFORMATION FOR SEQ ID NO: 4904:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4904:

25 TAAGTTGGCT ACCATCGACG CTAAGAACCT TTCTTGACTT GTGACAAATCG CTTGCTTCTT 60
 TCCTCTCTCT GGCTCTGCTT CTATTGCCT CTAATGTGGC TTTTGTGTGT AATAAGTTAT 120
 GCGCTTCGGT GTTATnGTGA AAAAGCGGTC A 151

30 (2) INFORMATION FOR SEQ ID NO: 4905:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4905:

40 TGACTTGTAG GCGCTGGTGG GATACTACCC TAGCTGTGTT GGCTTTCTAA CCGCACCAC 60
 TTATCGTGGT GGGGA 75

45 (2) INFORMATION FOR SEQ ID NO: 4906:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4906:

55

ACTCAGACAG TGA CT CAGAT CAGATAGT G_n CTCGGATTCA GCGATTATTC AG

112

(2) INFORMATION FOR SEQ ID NO: 4907:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4907:

15

GTAAAAACAC CCCAGCCAGG TCACTTTACG CCTACGCATC GCTTGATACAC GTGCTACTAA
 AGGTTTACCA

60

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(2) INFORMATION FOR SEQ ID NO: 4908:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4908:

30

AGAAGATACA AATAAAGnTA AACCCAAATT ATTCAATTTT GGTGGGACAC AATAGTGTGG
 ACTTTGAAGA AGATACACTT TCCACCAAG TTAAGTGGGT CCATAATTGA AGGGTCCAAC
 C

60

120

121

35

(2) INFORMATION FOR SEQ ID NO: 4909:

40

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4909:

50

GGGAACAAAG TGGACAGGTG GTGCATGGTT GTCGICAACT CGTGTCGTGA GATGTTGGGG
 TTAAGTCCCG

60

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(2) INFORMATION FOR SEQ ID NO: 4910:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4910:

GGACACCCGG AGAACTGAAA CATTAGTAC CCGGAGAAGA GAAGAAATTC GTTCCCTTAG 60
 TAGCGGGACG AACGGGAGAG CCCAAACCAC AGCTTGTGnG 100

(2) INFORMATION FOR SEQ ID NO: 4911:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4911:

nTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGCTA TAGTACCAG ACAAAATAAC 60
 TTACTTATTC ATGATACAG CTTAATTAAT AAGGTGCAAT AGTTAATTTT ACACITTTAG 120
 GTAAACTTTG GCACATCAGC TTTTAGTGTG TTTTCG 155

(2) INFORMATION FOR SEQ ID NO: 4912:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4912:

CCCGTCACAC CACGAGATTT GTAACACCG AAAGCCGGTG GAGTGAACCT TTTAGGAGCT 60
 AGCCGTCGA 69

(2) INFORMATION FOR SEQ ID NO: 4913:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4913:

TATGCTCTCC CAGCTGAGCT AATTCTCCGA TTAAAACTG CCTGGCAACG TTCTACTCTA 60
 GCGGAACGT 69

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4914:

CAAATGCTTC TGTCAATTCG ATCAAATCAA TGTCTTCAAC AGATAGATTG CTGAGTGACA 60
 ATACTTCAT 69

(2) INFORMATION FOR SEQ ID NO: 4915:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4915:

TATTTCGGAG AGAACCAGCT ATTCCAGGC TCGATTGGAA TTCTCCGGT ACCCTCAGTT 60
 CATCCGCTCA 70

(2) INFORMATION FOR SEQ ID NO: 4916:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4916:

TCACCCATTA ACGGGCTCTA ACTACTTGTA AGCACACGGT TTCAGGTCT ATTCACTCC 60
 CCTTCCG 67

(2) INFORMATION FOR SEQ ID NO: 4917:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4917:

TCCACCGTTG ACTAAGGTTT CAGAGAGGCT CGTCCCTCTG GGTAGTCGGG CCTAAGCTGA 120
 GCGCGACGTA GCGGATGATA CAGGTTATAT CCTACACCT A 161

5 (2) INFORMATION FOR SEQ ID NO: 4918:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4918:

GCACGTAGTT AGCGTTGGC TTTCTGATTA GGTACCGGCA AGATGTGCAC AGTTACTTAC 60
 ACATATGT 68

20 (2) INFORMATION FOR SEQ ID NO: 4919:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4919:

30 GAAAGCAAAT GTCTTCGTTG CAATTCGATC AAATCAATGT CTTCAACAGA TAGATTGCTG 60
 AGTGACAATA CTTCAGGG 78

35 (2) INFORMATION FOR SEQ ID NO: 4920:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4920:

45 AATTTCGCTA CCTTAGGGAC CGTTATAGTT ACGGCCGAGC TTACTGGGG CTTGATTTCG 60
 TACTTCGC 68

50 (2) INFORMATION FOR SEQ ID NO: 4921:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4921:

5 AATCATAGTA CCTGTAAAGA TGCAGGTTAC CCGCAACAAG ACGGAAAGAC CCCGTGGAGC 60
TTTACTG 67

(2) INFORMATION FOR SEQ ID NO: 4922:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4922:

20 GGGAGCTGTA ATAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT 60
GTCATG 66

(2) INFORMATION FOR SEQ ID NO: 4923:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4923:

35 GTGGAGGCGC TGGTGGGATA CTACCCTAGC TGTGTGGCT TTCTAACCG CAACCACTTA 60
TCGTGGGTGG GAG 73

(2) INFORMATION FOR SEQ ID NO: 4924:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4924:

50 GAGGTCAGCG GTTCGATCCC GCTAGTCTCA CCATTATT TTTACACGAT GACATGAAAC 60
TGATGACATA TGCACCGTAA TTCCAAAAA 89

(2) INFORMATION FOR SEQ ID NO: 4925:

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- (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4925:

10 AATGGCATCG GAGTGTGCTG AATTCGGTAA CCCGAGAGGC CCTCGTGCCA AACAGGCTCT 60
 ACCTCCAA 68

(2) INFORMATION FOR SEQ ID NO: 4926:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4926:

25 ACGAAAGGCG TAACGATTG GCACTGATC TCGACGAGAG ACTCGTGAAA ATCATAGATA 60
 CCTGTGAAGA TGC 73

(2) INFORMATION FOR SEQ ID NO: 4927:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4927:

40 ATTTCTATTA ATTATTIGCA TAGAAATCAG CTTTTTIGAT ATGTATTITTA TAATGTACAG 60
 CTCGTTGAG 69

(2) INFORMATION FOR SEQ ID NO: 4928:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4928:

55 AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACATCTC CTCTCAAATT TCCTACGCC 60

(2) INFORMATION FOR SEQ ID NO: 4929:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4929:

GGCGGGGCCC CAACACAGAG GCTGGCGGAA AGTGCAGCTT ACAATAGTGT GCAAGTTGGG 60
 GTGGGTCCCG ACACAGAGAA ATT 83

(2) INFORMATION FOR SEQ ID NO: 4930:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4930:

CITGGTAGAG CACTTGGTTT GGGACCAAGG GGTGCGAGTT CGAATCCTGT CTTCCCGATT 60
 ACTCTA 66

(2) INFORMATION FOR SEQ ID NO: 4931:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4931:

AAGAAGCTTG TTATGCTGCA ACACCAGCAA TTCAAGTAGC TAAAGATTAT TTAGCAACTA 60
 GACCG 65

(2) INFORMATION FOR SEQ ID NO: 4932:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

	TGCAGAAGAG GAAAGTGGAA TTCCATGTGT AGGGTGAAAT GGCATAGAT ATGGCAGGAA	60
	CACCACTGGG CGA	73
5	(2) INFORMATION FOR SEQ ID NO: 4933:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 65 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4933:	
	TCGCTATCCG AGTCTGGGTC GCTATCTGAG TCTGAGTCG TATCTGAGTC TGAATCGCT	60
	GTCTG	65
20	(2) INFORMATION FOR SEQ ID NO: 4934:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 120 base pairs	
	(B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4934:	
	GAGCATGTGG GTTTAATTCG AAGCAACGCA GAGAACCTTG ACCAAATCTT GGACATCCnT	60
	TGACAACTCT GAGAGATTAG AGCCTTGCCC CTTCGCGGGT AACAAATGTA CAGGTTGGTG	120
35	(2) INFORMATION FOR SEQ ID NO: 4935:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 72 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4935:	
	GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA GGCCGAGCAG GTACGCGAT	60
	GSATAACGGT TG	72
50	(2) INFORMATION FOR SEQ ID NO: 4936:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 64 base pairs	
	(B) TYPE: nucleic acid	
55	(C) STRANDEDNESS: double	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4936:

5 CACATCAGCG TCAGTTACAT ACCAGAAAGT CGCCTTCGCC ACTGGTGTTC CTCATATCT 60
CTGC 64

(2) INFORMATION FOR SEQ ID NO: 4937:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4937:

ATCACCTGGT GTAAACCAAT TAGTACGTGT ATATATCGTT CAAAACCGTA AAATTCATGT 60
20 TGGT 64

(2) INFORMATION FOR SEQ ID NO: 4938:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4938:

CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAACATC TAAGCATGAA GCCCCCTCAA 60
35 GAT 63

(2) INFORMATION FOR SEQ ID NO: 4939:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4939:

TAGAAATCAG CTTTTTTCGA TATGTATTTT ATAATGTACA GTCGTTGAG CTGCTATTTT 60
CCT 63

50 (2) INFORMATION FOR SEQ ID NO: 4940:

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- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4940:

GGTAGTCGAA CTTACGTTCC GCTAGAGTAG AACTTGCCAG CAAATGACAA ATCGAGAAAT 60
TAGCTCAG 68

(2) INFORMATION FOR SEQ ID NO: 4941:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4941:

CTGAACATC TTAGTACCG GAGAAGAGAA AGAAAATTCG ATTCCCTTAG TAGCGCGAG 60
CG 62

(2) INFORMATION FOR SEQ ID NO: 4942:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4942:

TTACAACAAT GCAATTGGCG GGGCCCAACA TAGAACTGGC AATAGTTACT TTCAATAATG 60
TGCAAGTTGG GGTAGGGCCC AACACAGAA 89

(2) INFORMATION FOR SEQ ID NO: 4943:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4943:

AATGGACAAT ATGTCACGT TAATTCCAAA AAACGGTAAC TATAATTAC AAACATTATT 60

55

(2) INFORMATION FOR SEQ ID NO: 4944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4944:

CCCGTGAAAG ATGATGAGGT TAATAGGTTT GAGGTGGAAG CATGGTGACA TGTGGAGCGT 60
GACGAATACG TAATTGA 77

(2) INFORMATION FOR SEQ ID NO: 4945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4945:

GAATAGGTCG ATGTATTGG CGACCGAAAC CAGGAATCTA CCCTTGGTCA GGTTGAAGTT 60
CAGGTAACAC TGAAT 75

(2) INFORMATION FOR SEQ ID NO: 4946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4946:

ATCAGAAGGC ACACCCGAGA ATGAAACATC TAGTACCCGG AGAAGAGAAA GAAATTCGAT 60
TCCCTATAGC GCGGCGGAAA CGGAAGAGCC AACCACAGCT GCTTTGGTTT GACCCATCGG 120
TACAGCGCTG ACACT 135

(2) INFORMATION FOR SEQ ID NO: 4947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4947:

GATTTGGGCT CTTCATTTC GCTCGCCGCT ACTAAGGGAA TCGAATTTC TTTCTCTTC 60

T 61

(2) INFORMATION FOR SEQ ID NO: 4948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4948:

GCTTTTGAGG AATTTAATAT CAATATATAT TCTGTGTATG AAAATATTTT TCATAAAAAAT 60

TGTTTGAATC 70

(2) INFORMATION FOR SEQ ID NO: 4949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4949:

CITCGACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACCAAGT ACTAAACGCC 60

CTATTC 66

(2) INFORMATION FOR SEQ ID NO: 4950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4950:

GGGTGTTACA AAATATCGTG GTGTGACGGG GCGGTGTGTA CAAGACCCCG GGTACGTTTT 60

TCACCGTAGG CATGCTGG 78

(2) INFORMATION FOR SEQ ID NO: 4951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4951:

CCGCGATAAT AAAAAATAAT GGCGGAGGAA GAGGGATTG AACCCTCCGTG GCCCGTTAAG 60

10

G 61

(2) INFORMATION FOR SEQ ID NO: 4952:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4952:

ACTTATCTAG TTTCAATGT ACAATGTCTT TTAGTCAGC GCTCGCATAA GCAATATCAC 60

25

TGTAACCA 68

(2) INFORMATION FOR SEQ ID NO: 4953:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4953:

ACTGACGCTG ATGTGCGAAA GCGTGGGGAT CAAACAGGAT TAGATACCCCT GGTAGTCCA 59

(2) INFORMATION FOR SEQ ID NO: 4954:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4954:

CGTGAGCGCT AGCTGTACGT GGAGCGCTG GTGGGATACT ACCCTAGCTG TGTGGCTTT 60

(2) INFORMATION FOR SEQ ID NO: 4955:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 59 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4955:

AAGGCGTAAC GATTTCGGCA CTGTCTCAAC GAGAGACTCG GTGAAATCAT AGTACCTGT 59

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(2) INFORMATION FOR SEQ ID NO: 4956:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4956:

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AATAGGTGCC CGTACGCCAA ACGACACAG GTAGTCAAGA TGAGAATTCT AAGGTGAGC 59

(2) INFORMATION FOR SEQ ID NO: 4957:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4957:

ACAGGTTTAG TTCACGCGGG TTTTGCTTGG TAAATCTAT ATTTACTTA CTTATCTAGT 60

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TTTCAATGTA CAATTTTC 77

(2) INFORMATION FOR SEQ ID NO: 4958:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4958:

TGTGTCGAGC TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCCTTAA 59

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(2) INFORMATION FOR SEQ ID NO: 4959:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4959:

GACTTGAACC CCCAACCTAC TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCGG

59

(2) INFORMATION FOR SEQ ID NO: 4960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4960:

TATTAACTGG TGACTTAGCG AGATGGACAA CGATGGCGAT ATATTTATTA TTGACCGCA

59

(2) INFORMATION FOR SEQ ID NO: 4961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4961:

ATGATTATCA TATTGCCTTA AATATCGCCA CAATTTTAGC GGGTGGTGAT TTACCAAGA

59

(2) INFORMATION FOR SEQ ID NO: 4962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4962:

CGCCGAAAAT TGTACCGGGG CTAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACA

59

(2) INFORMATION FOR SEQ ID NO: 4963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TTAAGCTTAG TTGCCATCAT TAAGTTGGGC ACTCTAATGT TGACTGCCGG TGACAAACCG 60

(2) INFORMATION FOR SEQ ID NO: 4964:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4964:

TAGTTTGGT ACGGTAACAA ATTTATTGA AGAAACAATC TCAAATAAAG AATTGTTG 59

(2) INFORMATION FOR SEQ ID NO: 4965:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4965:

AGTTCGGTCC CTATCCGTCG TGGGGCGTAG GAAATTTTAG AGGAGCTGTC CTTAGTACG 59

(2) INFORMATION FOR SEQ ID NO: 4966:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4966:

TACAAAGGGC AGCGAAACCG TGAGTCAAAG CAAATCCCAT AAAGTTGTTT TCAGTTCGG 59

(2) INFORMATION FOR SEQ ID NO: 4967:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4967:

CCATTGCAGC ACCGACAGCC ACACCATTTA TTTTTCGCT ATGTATATCG CATTAAACGT 60

(2) INFORMATION FOR SEQ ID NO: 4968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4968:

GCCTCCGTTA CTTTATGAGG CGACGCCAG TCAAACTGCC CGCTGACACT GTCTCCACC 60

(2) INFORMATION FOR SEQ ID NO: 4969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4969:

CAAGGAATTT CGCTACCTTA GGACGGTTAT AGTTACGGCC GCCGTTTACT GGGGCTTCG 59

(2) INFORMATION FOR SEQ ID NO: 4970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4970:

CATCTGTCAC AGGTACTATG GATTTCACCG GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60

TTACG 65

(2) INFORMATION FOR SEQ ID NO: 4971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4971:

CTAGAGTTGG CATACCAGTC CGTCGCTAAG GAACCTTTCT TGACTTGATG ACAATCGACT 60

(2) INFORMATION FOR SEQ ID NO: 4972:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4972:

AGACCCCGTG GAGCTTTACT GTAGCCTGCA TATTCGAATT CGGCACAGCT TGTACAGGAT 60
 AGGTAGG 67

(2) INFORMATION FOR SEQ ID NO: 4973:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4973:

TGTGTACTTA AAAATATGAA TACATGAGTA AAACATGTC ATAAGAAATA CTAATTTC 58

(2) INFORMATION FOR SEQ ID NO: 4974:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4974:

ACCTCCAATA ATCATCACTT GAGGCTAGCC CTAAGCTAT TTCGGAGAGA ACCAGCTA 58

(2) INFORMATION FOR SEQ ID NO: 4975:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4975:

GAGCCACAT CCTTTCCAC TTGGCGTGTG TTTTGGGACC TTGGCTGGTG GTCTGGGCTG 60

(2) INFORMATION FOR SEQ ID NO: 4976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4976:

TCACTAAGTC CGTCTTCGA CCCTGACTCG ACTGTAGGT CTCGCAGTCA AGCTCCCTT 59

(2) INFORMATION FOR SEQ ID NO: 4977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4977:

TAAGTAAGTA AATATAGAT TTTACCAAGC AAAACCGAGT GAATAAGAG TTTTAAAT 58

(2) INFORMATION FOR SEQ ID NO: 4978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4978:

GTGAGGTACG TCCAGAATGG GGATTGGCTA AAAATGCATC ATTTATAATT GGACGACG 58

(2) INFORMATION FOR SEQ ID NO: 4979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4979:

TCGCTATCTG AATCCGAGGT CGCTATCCGA ATCTGGAGTC GCTATCTGGA GTCTGGAATC 60

(2) INFORMATION FOR SEQ ID NO: 4980:

(A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4980:

10 AAGAAGGTAA TAATCTGTGA GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGAGTAC 58

(2) INFORMATION FOR SEQ ID NO: 4981:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4981:

20 GTGGTGTGTT AGGGCACTCT ATACGGGTGA CAAAGTACGA CATTAGACGG ATCATCTGGA 60

25 AAGATGAATC AAAGT 75

(2) INFORMATION FOR SEQ ID NO: 4982:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4982:

35 GTTTTCATT TCAATTATA TTIATATTAG TGTTAATCCA ATCATAGATT TATCTATA 58

(2) INFORMATION FOR SEQ ID NO: 4983:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4983:

50 TGACAGCTAA CTATTGGCCA GCTTCTATGT TGGGGCCCCG CCAACTTGCA TTGTCIGTAG 60

A 61

(2) INFORMATION FOR SEQ ID NO: 4984:

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(A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4984:

10 GGTGTTTTTA AGTCTGATGT GAAAACCCAC GGCTCAACCG GTAGAGGTCA TTGGAAACTG 60
 GAAA 64

(2) INFORMATION FOR SEQ ID NO: 4985:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4985:

25 CAGCATACAA TAATGTGCAA GTTGTCTGGG GCCCAACAT AGAGAATTC AAAAGAAAT 59

(2) INFORMATION FOR SEQ ID NO: 4986:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4986:

TGATGAAGGT CTTCGGATCG TAAACTCTG TTATTAGGGA AGAACATATG TGTAAGT 57

(2) INFORMATION FOR SEQ ID NO: 4987:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4987:

50 AAAGAATTG CGCAAAACGC TATCGATACT GAAGGGCGIT CAATGATTAT CATGGGT 57

(2) INFORMATION FOR SEQ ID NO: 4988:

55

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4988:

TTGTACAAG TCAAGAAAGG TCTTAGCGA CGATGGTAGC CAACTTACGT TCCGCTA 57

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(2) INFORMATION FOR SEQ ID NO: 4989:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4989:

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TAGGACCGTT ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAG 57

(2) INFORMATION FOR SEQ ID NO: 4990:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4990:

AAAGTCAACG TTAATTCCAA AAAACGTAAC TATAAGTTAC TAACATTATT TAGTATTTAT 60

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G 61

(2) INFORMATION FOR SEQ ID NO: 4991:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4991:

TCCACGGGGT CTTCCATCC TGTCTCGGGT AACCTGCATC TTCACAGGTA CTATGATTTT 60

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ACCGA 65

(2) INFORMATION FOR SEQ ID NO: 4992:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4992:

GTGCGGCTGG ATCACTCTCT TTCTAAGGAT ATATTCGGAA CATCTTCTTC AGAAGAT 57

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(2) INFORMATION FOR SEQ ID NO: 4993:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4993:

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CCAATGCGGC TCATCGCATC CATTITTTTGC CTGGCAACGT TCTACTCTAG CGGAACG 57

(2) INFORMATION FOR SEQ ID NO: 4994:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4994:

CTGTTTTCGG GTCTACGACA AATACTAAAC GCCTATTTCAG ACTCGCTTTC GCTACGG 57

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(2) INFORMATION FOR SEQ ID NO: 4995:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4995:

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CAAACTCTCG TGGTGTGACG GCGGTGTGG TACAAGCCCC GGGAACGTAT TCACCGTAGC 60

ATCCCGGTCT ACG 73

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(2) INFORMATION FOR SEQ ID NO: 4996:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4996:

ACTAATTTC ATAGGAAAAG TATCTTTAT CGTCGTCCCA CCCCAACTCG CACATTATTG 60
TAAGC 65

(2) INFORMATION FOR SEQ ID NO: 4997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4997:

ATTGGATTCC CAATTCTAC AGACAATGCA GTTGGGGTGG GACGTCGAAA TAAATTTT 58

(2) INFORMATION FOR SEQ ID NO: 4998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4998:

AACTTCAACA GGTTTTCAG GTGGCGGTGC GACTGCAGGA AGACGTAAAA TTAATG 56

(2) INFORMATION FOR SEQ ID NO: 4999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4999:

GGGCAGGCGT CAGCCCTATA CATCACCTTA CGGTTTAGCA GAGACCTGTG TTTTGT 56

(2) INFORMATION FOR SEQ ID NO: 5000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5000:

TTAGGACCCG ACTAACCCGAG AGCGGACGAG CCTTCCTCTG GAAACCTTAG TCAATC 56

5

(2) INFORMATION FOR SEQ ID NO: 5001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5001:

GACGGGATTC TCACCCGTCT TCGCTACTC ACACCGGCAT TCTACTTCT AAGCGC 56

15

(2) INFORMATION FOR SEQ ID NO: 5002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5002:

CCTGTCGGCC TCAGCTTAGG ACCCGACTAA CCCAGAGCGG ACGAGCCTTC CTCTGG 56

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(2) INFORMATION FOR SEQ ID NO: 5003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5003:

TTACTCATTT AGTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCA 56

40

45

(2) INFORMATION FOR SEQ ID NO: 5004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5004:

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(2) INFORMATION FOR SEQ ID NO: 5005:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5005:

GACATAGATT AAGTTATTAA GGGCGCACGG TGGATGCCTT GGCAC TAGAA GCCGATG 57

(2) INFORMATION FOR SEQ ID NO: 5006:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5006:

OGAACCCTA CATAATAAAT CATTAGTGGC TCTTTATCAT TCTGTCCAC TCCCTG 57

(2) INFORMATION FOR SEQ ID NO: 5007:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5007:

CGCTACGTTT TTCCTCAACA TTAAAGAAAA TAAAGAATGC TACAATTACG ATTGCAATCA 60
 AACCAAAGA 69

(2) INFORMATION FOR SEQ ID NO: 5008:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5008:

AAAAGCTTGT TACAAGCGCT ATTTTCGTTT AGTCAACTAC TGCCAATATA ACTTCGT 57

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5009:
 ACATCTTAGT ACCCGGAGAA GAGAAAGAAA ATTCGATTCC CTTAGTAGCG GCGAGC 56

(2) INFORMATION FOR SEQ ID NO: 5010:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5010:
 GTTTGGACGA GGGGCCCTCT CGGGTTACGA TTCAGACAAA CTCGATGCA ATTAATTTAC 60
 TTGGG 65

(2) INFORMATION FOR SEQ ID NO: 5011:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5011:
 TTTACTTGTA TTGGAATAAT TTCATCTTGG AACCGACCAT CAGTTGTGC GTCATA 56

(2) INFORMATION FOR SEQ ID NO: 5012:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5012:
 CCTTATACAT CACCTTTACG GTTTAGCAG AAACCTGTGT TTTTGATAA ACAGTCGCTT 60

(2) INFORMATION FOR SEQ ID NO: 5013:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5013:

10 GGGCCCAACA CAGAAGCTGG CGAAAAGTCA GCATACAAA TTGTGCAAGT TGGCGGGTCC 60
ACA 63

(2) INFORMATION FOR SEQ ID NO: 5014:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5014:

25 TAGGGTAGTA TCCACCACT GGCCTCCAG TAAGCTAGCG CTCACGTTT CAAAGGCT 58

(2) INFORMATION FOR SEQ ID NO: 5015:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5015:

CAACTCCGAT GCAATTAATT TAACCTGGGA nCAGACATGG GTGATAAGGT CGTGTTTCGAA 60
40 GGGAACAGCC AGACACAGCT AAGTCCAGAT ATATGTAAGT GGAAG 105

(2) INFORMATION FOR SEQ ID NO: 5016:

45

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5016:

CAAACGATTT ATTATATGTC TTATTTCITT ATTATTATT ATTACAATTA CATTTT 56

55

(2) INFORMATION FOR SEQ ID NO: 5017:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5017:

10 TCTGTAGAAA TTGGGGAATC CAATTTCCTCT TGGTTGGGT CCCATCCCA ACTTGACAT 60
 TATTG 65

(2) INFORMATION FOR SEQ ID NO: 5018:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5018:

25 GGGGATGGGC CCCAACAAAG AGAAATTTGA TTCCCAATTT CTACAGACAA TGCAAC 56

(2) INFORMATION FOR SEQ ID NO: 5019:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5019:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAATCCGG TACTC 55

40

(2) INFORMATION FOR SEQ ID NO: 5020:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5020:

50 TAGCGCGTTT AGTATTTGGT CGTAGCCGGA AACCAGGTGA TCTACCCTTG GTCAGTT 58

(2) INFORMATION FOR SEQ ID NO: 5021:

55

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5021:

TTGTGCGGGT CCCCGTCAAT TCCTTTGAGT TTCACCTTG CGGTCGTACT CCCCCA

55

10

(2) INFORMATION FOR SEQ ID NO: 5022:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5022:

20

AGAGTTCACA TCGACGGGGA GGTTTGGCAC CTCGATGTCG GCTCATCGCA TCCTG

55

(2) INFORMATION FOR SEQ ID NO: 5023:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5023:

CCTTAGCTGG TGGTCTGGGC TGTTCCCTT TCGAACACGG ACCTTATCAC CCATGGTC

58

35

(2) INFORMATION FOR SEQ ID NO: 5024:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5024:

TAAAGGCTAA ACTACCAATG TTITCAATGG ATITCCAAAA TGAATCATCT GGGAT

55

(2) INFORMATION FOR SEQ ID NO: 5025:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5025:

TCAAACCGGA GGGGTCATTG GAAACTCGAA AACTTGAGTG CAGAAGAGGA AAGTGGAATT 60

5 CCA 63

(2) INFORMATION FOR SEQ ID NO: 5026:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5026:

GCTTGC GTAC CTAAGAGCA CCCCTTCTCC GAATTACGGG GTCATTTTGC CGAGTTCCTT 60

20 AACG 64

(2) INFORMATION FOR SEQ ID NO: 5027:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5027:

AATACATAGC ATATCATAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGA 56

35 (2) INFORMATION FOR SEQ ID NO: 5028:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5028:

GGGCCCTCT CGGGTTACCA ATTCAGACAA ACTCCGAATG CCAATTAATT TAACT 55

(2) INFORMATION FOR SEQ ID NO: 5029:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5029:
 5 CGTAACTATA ACGGTCCTAA GTAGCCGAA ATTCCTTGTC GGGTAAGTTC CGAC 54

(2) INFORMATION FOR SEQ ID NO: 5030:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5030:
 15 ATCCCCGGGG CCCCAACACA GAGAATTTCG AAAAGAAATT CTACAGGCAA TGCAAGT 57

(2) INFORMATION FOR SEQ ID NO: 5031:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5031:
 25 TGCCTGGTAA AATCTATAIT TTACTACTT ATCTAGTTTT CAATGTACAA TTTC 54

(2) INFORMATION FOR SEQ ID NO: 5032:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5032:
 40 TCCCTATCCG TCGTGGGCGT AGGAAATTG AGAGGAGCTG TCCTTAGTAC GAGA 54

(2) INFORMATION FOR SEQ ID NO: 5033:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5033:
 55

(2) INFORMATION FOR SEQ ID NO: 5034:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5034:

TAITCTGAATC TGAGTCGCTG TCTGAATCTG AATCGCTATC CGAGTCTGAG TCGC

(2) INFORMATION FOR SEQ ID NO: 5035:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5035:

CACCAGCAAT TCAATTAGCT AAAGATTATT TAGCAACTAG ACCGGAATGA AAAA

(2) INFORMATION FOR SEQ ID NO: 5036:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5036:

CTACCATCGA CGCTAAGAGC TTAAC TTCTG TGTTCCGGCAT GGGAACAGGT GTGA

(2) INFORMATION FOR SEQ ID NO: 5037:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5037:

CGGCCGAGTTA CGATTGTATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG CGGAAG

(2) INFORMATION FOR SEQ ID NO: 5038:

(A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5038:

10 GACCGGGATG GACATACCTC TGGTGACCA GTTGTGCTG CCAACGCATA AGCT

54

(2) INFORMATION FOR SEQ ID NO: 5039:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5039:

TTTACCGGAG TCTCTCGTTG AGCAGTCCCC AAATCGTTAC GCCTTTCGTG CGGG

54

25

(2) INFORMATION FOR SEQ ID NO: 5040:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5040:

35

TTATAACACG TATGCTTGGG GAGTGTAAATA AGCTTGATCA GAGATTCCnA TGGGAACCAG

60

CATGAGTTAT GTCATTATC ATATGTGATC ATAGCATATC AAAGG

105

40

(2) INFORMATION FOR SEQ ID NO: 5041:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5041:

50

GGCACCTATT TTCTATCTAG AGGCTTTTCT CGGCAGTGTG GAAATCAACG ACTC

54

(2) INFORMATION FOR SEQ ID NO: 5042:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 54 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5042:

ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCG

54

10

(2) INFORMATION FOR SEQ ID NO: 5043:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5043:

20

CGTTCAGTCA ACTACTGCCA ATATAACATC GTAGAGCATA GAACATTGAT TTA

53

(2) INFORMATION FOR SEQ ID NO: 5044:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5044:

ACTAGAGAGT ATTAGACTT AGGAGTGGTC CTCCAGATT CCGACGGATT TCACGTGCT

35

59

(2) INFORMATION FOR SEQ ID NO: 5045:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5045:

45

TTTCGTCGTC CCACCCCAAC TTGCACGCTA TTGTGAGCTG ACTTTTCGCC AGCTTCTGTG

60

TT

62

50

(2) INFORMATION FOR SEQ ID NO: 5046:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5046:

5 CGTCATCCCC ACCTTCCTCC GGTITGTCCAC CGGCAGTCAA CTTAGAGTGC CCA 53

(2) INFORMATION FOR SEQ ID NO: 5047:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5047:

TATTATTAA ACCTAATAAA GATGAATTAG AAGTGATGTT TAATACAACA GTG 53

(2) INFORMATION FOR SEQ ID NO: 5048:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5048:

30 CCTCGGCACC ATTTCAATA AAAACATATG CGCCCGTAGC TCAATTGGAT AGA 53

(2) INFORMATION FOR SEQ ID NO: 5049:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5049:

AAATGGCCAA CTTAAGCCAG GATACAATT ACAAAATAGCG ACAAAATTCTC AATGTGTTT 59

45 (2) INFORMATION FOR SEQ ID NO: 5050:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

CGAAAGACAC nCACAAGATT AATAACGCGT TTGAGTCTTT TTATAAGAC GTACTTCATG 60
 TTACGTTGAC TTTAAGATGG TGGACATAG TTAGTTTATG GGCCACGGG G 111

5 (2) INFORMATION FOR SEQ ID NO: 5051:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5051:

15 ACGTTGACAT ATTGTCAATC AGTTTTCAAT GTTCATTAAT GTTCAATCTC TTT 53

(2) INFORMATION FOR SEQ ID NO: 5052:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5052:

25 CTGAATTCGG TAACCCGAGA GGGCCCCCTG TCCAAACAGT GCTCTACCTC CAA 53

30 (2) INFORMATION FOR SEQ ID NO: 5053:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5053:

40 TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC CGG 53

(2) INFORMATION FOR SEQ ID NO: 5054:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5054:

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(2) INFORMATION FOR SEQ ID NO: 5055:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5055:

TAGGGCTAGC CTCAAGTGAT GATTATTGGA GGTAGAGCAC TGTTGGACG AGG 53

(2) INFORMATION FOR SEQ ID NO: 5056:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5056:

ACTGCTTTGA AATGTTGTTG TCTCAGTTAA TATTCAATTG CTTTTCITTT GCATAATTGA 60
 CAA 63

(2) INFORMATION FOR SEQ ID NO: 5057:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5057:

CTATGTTGGG GCCCGCCAA CTGTCATTGT CTGTAGAATT CCTTTCGAA ATTC 54

(2) INFORMATION FOR SEQ ID NO: 5058:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5058:

CTGAATCCGA GTCGCTATCC GAGTCTGAGT CGCTATCTGA GTCTGAATCG CTG 53

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5059:
TTTGGGCTAC ACACTGCTA CAATGGACAA TACAAAGGCG AGCGAAACCG TGATGTCAA 59

(2) INFORMATION FOR SEQ ID NO: 5060:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5060:
AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT AAAAAACAGC AGT 53

(2) INFORMATION FOR SEQ ID NO: 5061:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5061:
TTAAGAGTGG CGTAATAGCT CACTAATCGA GTGACAATGG CGCCGAAAT GTACC 55

(2) INFORMATION FOR SEQ ID NO: 5062:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5062:
TACCAGGGTA TCTAATCCTG TTGATCCCC ACGCTTTCGC ACATCAGCGT CA 52

(2) INFORMATION FOR SEQ ID NO: 5063:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5063:

TCGCCAAGCC ATTTTCTTT GTGTTCTTT TTATTTGAC GTTTAGACA TA

52

10

(2) INFORMATION FOR SEQ ID NO: 5064:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5064:

20

CTCAAGCTCC CTGTGCCTT TACTCTTAT GTGTGCTTC CGACCGTTCT GGGGGGAAC

60

TTGAGCGCC TCCGT

76

25

(2) INFORMATION FOR SEQ ID NO: 5065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5065:

35

CCACCGCTTG TCGGGTCCC CGCAATTCC TTGAGTCGC AACCTTCGG TCGT

54

(2) INFORMATION FOR SEQ ID NO: 5066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5066:

45

TCCCGGGCT AACATATTA CCGAAGCTGT GGATGTCCT TTGACAATG GTAGG

55

50

(2) INFORMATION FOR SEQ ID NO: 5067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5067:

GCTCATCGCA TCCACTTTT GCTTGGCAAC GTTCTACTCT AGCGGAACGT AA

52

(2) INFORMATION FOR SEQ ID NO: 5068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5068:

CGGACACCAG AAGTACCAAG CGAGCCGGAA ACACCAACAC CACCGACACC AGACGTACAA

60

GCGAGCCGGAA ACAACACAA CG

82

(2) INFORMATION FOR SEQ ID NO: 5069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5069:

TCCATAACGT GCTGTATCTG TAGCAATAAC TAATACTTTT TCATTGCGTC TA

52

(2) INFORMATION FOR SEQ ID NO: 5070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5070:

CGACTCGAAG ACTCAATGTC TTCTCCCAT CACAGCTCAG CCTTAACGAG TA

52

(2) INFORMATION FOR SEQ ID NO: 5071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5071:

GCGATGGATA ACAGGTTGAT ATTCTGTAC CACCTATAAT CGTTTTAATC GA 52

(2) INFORMATION FOR SEQ ID NO: 5072:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5072:

CACTTCACCA CAGCCGCCAT GGCATGGCA GTAGGAATCG AACCCACACC AAA 53

(2) INFORMATION FOR SEQ ID NO: 5073:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5073:

GTCCAGACTC CTACGGGAGG CAGCAGTAGG GAATCTCCG CAATGGGCGA AA 52

(2) INFORMATION FOR SEQ ID NO: 5074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5074:

TGTTGGCTTA GAATCAGCCA TCATTTAAAG AGTGCCTAAT AGCTCACTAG TCGC 54

(2) INFORMATION FOR SEQ ID NO: 5075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5075:

AAACTTCCTCCT TTGG 74

(2) INFORMATION FOR SEQ ID NO: 5076:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5076:

TGAGCTAATC AGACATCATA ATTTTATGAG AGAGTTTGAT CCTGGCTCAA GAT 53

(2) INFORMATION FOR SEQ ID NO: 5077:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5077:

GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTT CGCTAGAGTA GA 52

(2) INFORMATION FOR SEQ ID NO: 5078:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5078:

GGGTAAGTTC CGACCCGCAC GAAAGGCGTA ACGATTGGG CACTGTCTCA AC 52

(2) INFORMATION FOR SEQ ID NO: 5079:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5079:

ATTAATCCAT TGTGCCACAA GTGCCGGACC AGAAATGATG GTATTTAATA AT 52

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5080:
 AATAGCGACG AATCACACCT TCTCGGCAC CACGGAATAA TACACCATGT GG 52

(2) INFORMATION FOR SEQ ID NO: 5081:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5081:
 CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAAGCGCTC CACATGTCCT TA 52

(2) INFORMATION FOR SEQ ID NO: 5082:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5082:
 CAGACAGCGA CTCAGATCAG ATAGCGATCG GACTCAGACA ACGACTCAGA TTCAGA 56

(2) INFORMATION FOR SEQ ID NO: 5083:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5083:
 AGGGTATGAT CCATCCCGGG TCCTCTCGGT ACTAAGGGAC AGCTCCTCTC AAATTTCCTA 60
 CG 62

(2) INFORMATION FOR SEQ ID NO: 5084:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5084:

10 GTGTACCACT GTGCTGCCA ACGGCATAGC TGGGTAGCTA TGTGTGGACG AG 52

(2) INFORMATION FOR SEQ ID NO: 5085:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5085:

TGCTTACGC TTGCTATAGC CAATATATAG ATGTTGGAGG GGGCAGATTG GAATGCGAAC 60

25

CCGAGGAGCG GATTAACA 78

(2) INFORMATION FOR SEQ ID NO: 5086:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5086:

ACTGACGCTG ATGTGCGAAG CGTGGGGATC ACACAGGATT AGATACCCTG GT 52

(2) INFORMATION FOR SEQ ID NO: 5087:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5087:

50 AAGTTGTTCT CAGTTCGGAT TGTAGTCTGC AACTCGACTA CATGAAGCTG G 51

(2) INFORMATION FOR SEQ ID NO: 5088:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5088:

ATACTTTAA AAAATAAGA CACTTTGGCC AACTTAAGCC AGGATACAAT T 51

10

(2) INFORMATION FOR SEQ ID NO: 5089:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5089:

20

AGAACGTAAA TTTAATCCTG ATTTAGCACC AGGGACAGAA AAAGTAACAA G 51

(2) INFORMATION FOR SEQ ID NO: 5090:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5090:

CCGCTACCCT CAGTTCATCC GTCACITTTT CAACGTAAGT CGGTTCGGTC C 51

35

(2) INFORMATION FOR SEQ ID NO: 5091:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5091:

45

CATGGGTGAT AAGGTCGGTG TTCGAAAGGG AAACAGCCCA GACCACCAG C 51

(2) INFORMATION FOR SEQ ID NO: 5092:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5092:

TTGTGCGGAT CCCGCTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCA 55

5 (2) INFORMATION FOR SEQ ID NO: 5093:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5093:

15 CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG A 51

(2) INFORMATION FOR SEQ ID NO: 5094:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5094:

ACGAATACTA ATCGATCGAA GACTTAATCA AAATAAATGT TTTGCGACAA A 51

30 (2) INFORMATION FOR SEQ ID NO: 5095:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5095:

40 AATCGTTGTT ACCTTCATTA TACCACTTAC TTGTGGAGTG ATCTTCTTCA AAGTAACACT 60

ATTGTGCCAC CGATTGA 77

45 (2) INFORMATION FOR SEQ ID NO: 5096:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

50 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

TTCGTAAGGA CATGIGSAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CG

52

(2) INFORMATION FOR SEQ ID NO: 5097:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5097:

15 GGGTCTGTTT TCTAATTGA GCACAATCTT CGTTCTCAAT AGAATGATTT A

51

(2) INFORMATION FOR SEQ ID NO: 5098:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5098:

CTGTAGAAAT TGGGAATCCA ATTTCTCTAT GTTGGGGCCC ACACCCCAAC T

51

(2) INFORMATION FOR SEQ ID NO: 5099:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5099:

40 CTGTGGATTG TCCTTGCCA TGAGATAGGA GAGCGTTCTA AGGCGTTGA A

51

(2) INFORMATION FOR SEQ ID NO: 5100:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5100:

GTTTCAGAAC GTCGTGAGAC AGTTCGTCC CTATCCGTCG TGGCGTAGG A

51

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5101:

TGACTGATAC GATCAATGCG CTTGTAACAA GCTTTTTC A ATTCTAGTCA GGGGCCCCAA 60
 CACA 64

(2) INFORMATION FOR SEQ ID NO: 5102:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5102:

TATTGCAATT TATATTGACG TTTTAAACAT AAAAAAAGAA ACCTTGCGGT CTCAATGG 58

(2) INFORMATION FOR SEQ ID NO: 5103:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5103:

ATTACCATT TGGTATACCA CATCGTTATT CAACACATTA TCTTTTACTT 50

(2) INFORMATION FOR SEQ ID NO: 5104:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5104:

GGACACTGCT CCTCAGGAG TCTCGCCATT AATACTACGT ATTAACATGT AAT 53

(2) INFORMATION FOR SEQ ID NO: 5105:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5105:

10 ATTCTCTCTT TTCTACAAT CGAGTCTCCT TTTACAGGTC CATAITTTGT

50

(2) INFORMATION FOR SEQ ID NO: 5106:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5106:

TGGTCAAGCG GTTAAGACAC CGCCCTTTCA CGCGGTAAC ACGGTTCTGA

50

25 (2) INFORMATION FOR SEQ ID NO: 5107:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5107:

35

TTTTTAGCAG TAATTGCCAC ATCTGTGTGA CGATAATGAT ATGCGACAGT

50

(2) INFORMATION FOR SEQ ID NO: 5108:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5108:

CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGACATAA

50

50 (2) INFORMATION FOR SEQ ID NO: 5109:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5109:

AGCCGATGAA GGACGTACT AACGACGATA TGCTTTGGGG AGCTGTAAGT 50

(2) INFORMATION FOR SEQ ID NO: 5110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5110:

ATCCATAACG TTGTGATCT GTAGCAATAA CTAATACTTT TTCATTCGGT CTA 53

(2) INFORMATION FOR SEQ ID NO: 5111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5111:

CCCTTAGTAC TGCAGCTAAC GCATTAAGCA CTCGCGCTGA GGAGTACGAC CTC 53

(2) INFORMATION FOR SEQ ID NO: 5112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5112:

GGAGTCAAAG TCGTTGCCT TACGCTTGG CTATAGCCCA ATATATAGAT 50

(2) INFORMATION FOR SEQ ID NO: 5113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

AGAnTTTCTT TTCGAAATTC TTTATGTTGG GCGCCCGCCA ACTTGCAATG

50

(2) INFORMATION FOR SEQ ID NO: 5114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5114:

GCTGTGATGG GGAGAAAGACA TTGTGCTTTC GAGTCGTTGA TTTCACACTG

50

(2) INFORMATION FOR SEQ ID NO: 5115:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5115:

CTTGATTAAC TCATTATCAA GTTATGCACG TGTAAATGAA TTCGGCTTTA TCGAA

55

(2) INFORMATION FOR SEQ ID NO: 5116:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5116:

GTACTTAAAA AATGAATACA TGAGTAAAGC TCATGGCATA AGAAATACTA

50

(2) INFORMATION FOR SEQ ID NO: 5117:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5117:

CAGAATCAGA TAGCGATCA GAATCAGATA GTGAGTCAGA TTCAGCAGTn

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5118:

CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACnAA

50

(2) INFORMATION FOR SEQ ID NO: 5119:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5119:

AATCGTCGAA ACTTAATCAA AATAAATGTT TTGCGACAAA TCACITTTAC TTACTATCTA

60

(2) INFORMATION FOR SEQ ID NO: 5120:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5120:

CCGAAGITTA CGGGTTCATT TTGCGAGTT CCTTAACGAG AGTTCGCTCG

50

(2) INFORMATION FOR SEQ ID NO: 5121:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5121:

ATAATCCTGT AGTCGAAAT GTTGCTCTC TTGAGTGGAT CCTTAGTACG CCGGGGCACG

60

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61

(2) INFORMATION FOR SEQ ID NO: 5122:

- (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5122:

10 TAGCGACTCA GATTGAGACA GCGATTGAGA CAGCGACTCA GACTCAGATA 50

(2) INFORMATION FOR SEQ ID NO: 5123:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5123:

TATTTGTAAA TGTATCCCTG GCTTAAGTTG GCATTTTTC ATATGGTCTT 50

25

(2) INFORMATION FOR SEQ ID NO: 5124:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5124:

CACGAGCTGA CGACAACCAT GCACCACCTG TCACTTTGTC CCCGAGAAG GTCTCTATCT 60

(2) INFORMATION FOR SEQ ID NO: 5125:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5125:

AGAACACATT GCGACTCTCG AGTCGTTGAT TTCACACTGC CGTAGTAAAA GCCTCTAGAT 60

50

AGAA 64

(2) INFORMATION FOR SEQ ID NO: 5126:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 57 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5126:

GGACGACATT AGACGAATCA TCTGGAAAAG ATGAGTCAAA GAAGGTAATA GTCCTGT

57

10

(2) INFORMATION FOR SEQ ID NO: 5127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5127:

20

GTCCTTAGTA CGAGATGACC GGGATGGACA TACCTCTGGT GTACCAGTTG

50

(2) INFORMATION FOR SEQ ID NO: 5128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5128:

GCCGATTITA GCAGTTGTG CTTCGTTCAA TTTATGGGG CCATTATGG

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(2) INFORMATION FOR SEQ ID NO: 5129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5129:

45

TCCACACATA GCTACCCAGT CTATGCCGTT TGCACTACAA CTGGTACACC A

51

(2) INFORMATION FOR SEQ ID NO: 5130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5130:
 5 CTCAGTTGGT TGAGCATCTG ACTTTTAATC AAAGGTCAA GGGTCGAATC CTCCTTT 57

(2) INFORMATION FOR SEQ ID NO: 5131:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5131:
 15 TGTATTTCAC TTCAATGTTA TCAATATTAG TGCCATCTAT GACATCTGCC A 51

(2) INFORMATION FOR SEQ ID NO: 5132:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5132:
 30 TCTGTAGTC GAACGTGTTG TCTCTCTGA GTGGATCCTG AGTACGACGG A 51

(2) INFORMATION FOR SEQ ID NO: 5133:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5133:
 40 ACTCAGACAT TGGATTGAGA TTCAGACAGC GACTCAGATT CAGATAGCGA CTCAGATTC 59

(2) INFORMATION FOR SEQ ID NO: 5134:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5134:
 55

(2) INFORMATION FOR SEQ ID NO: 5135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5135:

CAATACnAAG GGCAGCGAAA CCGTATTCA AGCAAATCCC ATAAAGTTGG

50

(2) INFORMATION FOR SEQ ID NO: 5136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5136:

GAAGCTGGCG AAAAGTCAGC TTACAAAATG TGCCAGTTGG CGGGGGCCCA AC

52

(2) INFORMATION FOR SEQ ID NO: 5137:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5137:

TTGTAAGGAA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGANT

50

(2) INFORMATION FOR SEQ ID NO: 5138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5138:

CTGTACAAGC TGTGCCGATA TTTCAATATC AnGnTACAGT AnAGTCCAC

50

(2) INFORMATION FOR SEQ ID NO: 5139:

(A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5139:

10 GGTCGAATC CTGTCTTCCC GATATACTGT AATTATTATG GGGGCTTTC TC 52

(2) INFORMATION FOR SEQ ID NO: 5140:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5140:

GGTACTGAAC CTATAAATG TATGATGCG GTCTCGAGGG AATCGAACCC AGATCT 56

25

(2) INFORMATION FOR SEQ ID NO: 5141:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5141:

35

AGGAGGCTCG TCCGCTCTAG GTTAGTCGGG TCCTAAGCTG AGGCCGACAG TA 52

(2) INFORMATION FOR SEQ ID NO: 5142:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5142:

CACGCTTTTC ACATCAGCGT CAGTTACAGA CCAGAAAGTC GCCTTCGCAC TGGTGT 56

50

(2) INFORMATION FOR SEQ ID NO: 5143:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5143:

CTCCTAAAC AATTACATC CAAACCTTCA TCACTCAGCG GCGGTGCTC CGTCAGCTTT 60

CGCCATTGCG AAGAT 75

(2) INFORMATION FOR SEQ ID NO: 5144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:

GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT 55

(2) INFORMATION FOR SEQ ID NO: 5145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:

GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG 53

(2) INFORMATION FOR SEQ ID NO: 5146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:

AGCTGTGGAT TGTCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T 51

(2) INFORMATION FOR SEQ ID NO: 5147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5147:

CTCTTTGATC CGTAGTCAAA CGCTCTATCC AATTGAGCTA CGGGCGCATA

50

(2) INFORMATION FOR SEQ ID NO: 5148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5148:

GAACTAATTC TCCAAATAA TGACTCCTAC AGGAACTCGA ACCCGTATAA CCGCCGTAAA

60

(2) INFORMATION FOR SEQ ID NO: 5149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5149:

AAAGCACACC CGGAAAAC TG AACATCTTA AGTACCCGGA GAAAGAGAAA

50

(2) INFORMATION FOR SEQ ID NO: 5150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5150:

GTAAGTTCGC ACTACCATCG ACGTAAGGG AGCTTAACIT CTGTGGTTCG GCATGG

56

(2) INFORMATION FOR SEQ ID NO: 5151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5151:

(2) INFORMATION FOR SEQ ID NO: 5152:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5152:

CTATTCTCTG TGTGGGGCTC ACCCCAACTT GCACACTATT GTAAGCTGAC TTTCCTCCA 59

(2) INFORMATION FOR SEQ ID NO: 5153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5153:

TAACCACATC ATTCGGATAC TGTTCATGGA AGTAATTCTT CTATTCTTCG GACCAGGAAA 60
 ATACA 65

(2) INFORMATION FOR SEQ ID NO: 5154:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5154:

CCATATGTGT CAGTCACTGT GCACATCTTG ACGGTACCTA ATCAGACAGC CACGGCTAAC 60
 TCCGTGCCAG CCGCCGCGGT ACTACGTGGT G 91

(2) INFORMATION FOR SEQ ID NO: 5155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5155:

(2) INFORMATION FOR SEQ ID NO: 5156:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5156:

GACTCTGGGA GGACCATCTC CTAAGGCTAA ACTACTCTCT CGTGACCGAT AGTGAACC 58

(2) INFORMATION FOR SEQ ID NO: 5157:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5157:

TTGTAACTCC GGTATAGGAG TGTCTTACAA CCCCAACAAG CAAGCTTGTT G 51

(2) INFORMATION FOR SEQ ID NO: 5158:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5158:

TAGThACCGn TAGTGAACCA TTACCGTGAG GGAAAGGTGA AAAGCACCCC 50

(2) INFORMATION FOR SEQ ID NO: 5159:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5159:

TTGCTCGCC GCTACTCAAG GGAATCGCAT TTCCTTTCTC TTCCTCCGGG T 51

(2) INFORMATION FOR SEQ ID NO: 5160:

(A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5160:

10 AACTGGAGAA ACACTTTAT GGGGTTTGCT TGAACCTCGC GGTTCGCTG CCCITTGTAT 60

T 61

(2) INFORMATION FOR SEQ ID NO: 5161:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5161:

25 AGACCTCTGC CTTACCACTT GGCTATGCGC CAATAACTGG GCTACCTGGA T 51

(2) INFORMATION FOR SEQ ID NO: 5162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5162:

35 CCGCTCACTT TTCAACGTAA GTCGGATCGG TCCTCCATTC AGTGTCACCT GAACT 55

(2) INFORMATION FOR SEQ ID NO: 5163:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5163:

50 CTTGATCTGT ATTTAAATG ATATTTTCTA TCTTTTCTTT ATTATTAAAG TCTATGACGT 60

CGTAGTATAA GATTCCGTGT A 81

(2) INFORMATION FOR SEQ ID NO: 5164:

55

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5164:

10 GTTCGAATCC CGTCTTCTGC TCCATTATT TGCCGGGGTG GCGGCAACTC TCACACGCAC

60

AG

62

(2) INFORMATION FOR SEQ ID NO: 5165:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5165:

25 CAGGGGTCTT TCGTCTGTG TGGGTAAC TG CATCTCACA GGTACTATGA TTCA

55

(2) INFORMATION FOR SEQ ID NO: 5166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5166:

35 AAGCTGAGGC CGACAGCGTA GCGATGGAT GACAGTTGA TATTGCCGGT ACCACCCGAT

60

40 AA

62

(2) INFORMATION FOR SEQ ID NO: 5167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5167:

50 CTTGCGTCTC CAGTTCGCC ACCCGGCAC TATAAAAATG GAGCAGAAGA CG

52

(2) INFORMATION FOR SEQ ID NO: 5168:

55

(A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5168:

10 TCGTCCGCTA TCCTCCACCAT TATTGTGACA TTGAACTAG ATAAGTAGTA AATATA

56

(2) INFORMATION FOR SEQ ID NO: 5169:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5169:

CTGTGCAGTC GGTGGGTAGT CGAACTTAC GTTCCGCTAG AGTAGAAGCT TGCCA

55

25

(2) INFORMATION FOR SEQ ID NO: 5170:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5170:

35

CTACTGCTGC ATATGCGGGT GAAGGAGTC GAACCCCCAC GCCGTAAGCA TA

52

(2) INFORMATION FOR SEQ ID NO: 5171:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5171:

GGGCTTnGGA CATTAGTTC TnAGGCAATG TAAAAAAGCT GATTTCATT

50

50

(2) INFORMATION FOR SEQ ID NO: 5172:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5172:

AAATTACATG TTAATACGTA ATTAATGGCG AGACTCCTGA GGAACCATTG CCATTCGAAG

60

(2) INFORMATION FOR SEQ ID NO: 5173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5173:

GTTTTATTTT TTAAAGTAT GTAAAGTAA AATTACATGn TAATACGTAn

50

(2) INFORMATION FOR SEQ ID NO: 5174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5174:

CAACTCTCGT TAAGGAAGTC GGAAAATAC CCGTAACCT CGGAGTAGGT CTCTTTA

57

(2) INFORMATION FOR SEQ ID NO: 5175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5175:

GGAACTGGA ATAAATAAC ATTCAATTGA GCGCATCAGT ATTAGGATTC ACTCTAAAAA

60

(2) INFORMATION FOR SEQ ID NO: 5176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GTAACGGACG CGCTCAAAGG TTCCTCACA ATGGTTGGAA ATCATTATA

50

(2) INFORMATION FOR SEQ ID NO: 5177:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5177:

AGTTACGTTT TTTTATAAGG AGGTTTGAGA CGCGTTATTA ATCTTGTGAG

50

(2) INFORMATION FOR SEQ ID NO: 5178:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5178:

GTGTGGATCC TGAGTACGAC GGAGCACGTG ACAATTCGGT CGGCAATCTG GGG

53

(2) INFORMATION FOR SEQ ID NO: 5179:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5179:

CGGTAACCTC ATACCTTTTA ACATATTTTG CATTGATTG CGTTTACCTT TTTTACCTTT

60

ACCGCCACCA GTGAACCTGTT TCA

83

(2) INFORMATION FOR SEQ ID NO: 5180:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5180:

TTTAAA

66

(2) INFORMATION FOR SEQ ID NO: 5181:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5181:

TTTCGGTAAC TCGAGCGGT CTCATAACCC GTAGTCGGG TGGTTCAAAT CCGTCCTCCC
 GCAATAT

60

67

(2) INFORMATION FOR SEQ ID NO: 5182:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5182:

TAGCGGTGAA ATGCGCAGAG ATATGGAGGA ACACCAGTAG CGAAGGCAAC TTTCT

55

(2) INFORMATION FOR SEQ ID NO: 5183:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5183:

GAATTCATG TGTAGCGGTG AAATGCGCAG AGATATGhAC GAACACCAAT

50

(2) INFORMATION FOR SEQ ID NO: 5184:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5184:

CC

62

(2) INFORMATION FOR SEQ ID NO: 5185:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5185:

GAGACCTTGT CGTCCATATG CGGGCTCATC GCATCCATTT TTTGCCTGGC AACGT

(2) INFORMATION FOR SEQ ID NO: 5186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5186:

CCATCATTAA GTTGGGCACT CTAAGTTGAC TGCCGGnGnC ACCnAAGAAG

(2) INFORMATION FOR SEQ ID NO: 5187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5187:

TTAATACGTT GCAATCCAAT CGCACGCTTC GCCTATCCTA CTGCCnTCCC

(2) INFORMATION FOR SEQ ID NO: 5188:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5188:

AGTCGCTATC CGAATCTGAG TCGCTATCTG AGTCnTAGTC GCTAnnCCAG

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5189:

ATAGATGCCC TTACCGCAAA CCGACACATG TAGTCAATAT GATAATTCTA AGGT

54

(2) INFORMATION FOR SEQ ID NO: 5190:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5190:

CTTTAATGGG CGAACAGnAC CCTTGGACCG ACTACAGCCC AGATCGATGA

50

(2) INFORMATION FOR SEQ ID NO: 5191:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5191:

ACATAGCACC CAGCGAGCCG TTGGACGACA ACTGGTACAC CAGAGGATGC CATCGGCCT

60

(2) INFORMATION FOR SEQ ID NO: 5192:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 320 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5192:

Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu
 1 5 10 15

		20		25		30	
	Leu	Ile	Ser	Ser	Lys	Ala	Gly
			35				40
	Val	Thr	Val	Ala	Asp	Thr	Met
					45		Lys
5							
	Lys	Ile	Gly	Lys	Asp	Gln	Ile
			50			55	Ala
	Asn	Ala	Asn	Ala	Ser	Phe	Thr
						60	Glu
							Met
							Leu
10							
	Asn	Lys	Ile	Leu	Ala	Asp	Lys
				70		Tyr	Lys
						75	Val
							Asn
							Asp
							Lys
							Lys
							80
	Ile	Asp	Glu	Gln	Ile	Glu	Lys
				85		Met	Gln
						Lys	Gln
						90	Tyr
							Gly
							Gly
							Lys
							Asp
							95
15							
	Lys	Phe	Glu	Lys	Ala	Leu	Gln
				100		Gln	Gln
						Gly	Leu
						105	Thr
							Ala
							Asp
							Lys
							Tyr
							110
	Lys	Glu	Asn	Leu	Arg	Thr	Ala
				115		Tyr	His
						Lys	Lys
						Glu	Leu
							Leu
							Ser
							Asp
							125
20							
	Lys	Ile	Lys	Ile	Ser	Asp	Ser
				130		Glu	Ile
						Lys	Glu
						135	Asp
							Ser
							Lys
							Lys
							Ala
							140
	Ser	His	Ile	Leu	Ile	Lys	Val
				145		Lys	Ser
						Lys	Lys
						155	Ser
							Asp
							Xaa
							Glu
							Gly
							160
25							
	Leu	Asp	Asp	Lys	Glu	Ala	Lys
				165		Gln	Lys
						Ala	Glu
						170	Glu
							Ile
							Gln
							Lys
							Glu
							175
30							
	Val	Ser	Lys	Asp	Pro	Ser	Lys
				180		Phe	Gly
						Glu	Ile
						185	Ala
							Lys
							Lys
							Glu
							Ser
							190
	Met	Asp	Thr	Gly	Ser	Ala	Lys
				195		Lys	Lys
						200	Asp
						Gly	Glu
							Leu
							Gly
							Tyr
							Val
							Leu
							205
35							
	Lys	Gly	Gln	Thr	Asp	Lys	Asp
				210		Phe	Glu
						Lys	Ala
						215	Leu
							Phe
							Lys
							Leu
							Lys
							220
	Asp	Gly	Glu	Val	Ser	Glu	Val
				225		Val	Lys
						Ser	Ser
						235	Phe
							Gly
							Tyr
							His
							Ile
							240
40							
	Ile	Lys	Ala	Asp	Lys	Pro	Thr
				245		Asp	Phe
						Asn	Ser
						250	Glu
							Lys
							Gln
							Ser
							Leu
							255
45							
	Lys	Glu	Lys	Leu	Val	Asp	Gln
				260		Lys	Val
						Gln	Lys
						265	Asn
							Pro
							Lys
							Leu
							Leu
							270
	Thr	Asp	Ala	Tyr	Lys	Asp	Leu
				275		Leu	Lys
						280	Glu
							Tyr
							Asp
							Val
							Asp
							Phe
							Lys
							285
50							
	Asp	Arg	Asp	Ile	Lys	Ser	Val
				290		Val	Glu
						295	Asp
							Lys
							Ile
							Leu
							Asn
							Pro
							Glu
							300
	Lys	Leu	Lys	Gln	Gly	Gly	Ala
				305		Gln	Gln
						310	Gly
							Gly
							Gln
							Ser
							Gly
							Met
							Ser
							Gln
							320

(2) INFORMATION FOR SEQ ID NO:5193:

(A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5193:

```

Met Asn Lys Val Ile Lys Met Leu Val Val Thr Leu Ala Phe Leu Leu
 1          5          10          15
Val Leu Ala Gly Cys Ser Gly Asn Ser Asn Lys Gln Ser Ser Asp Asn
15          20          25          30
Lys Asp Lys Glu Thr Thr Ser Ile Lys His Ala Met Gly Thr Thr Glu
20          35          40          45
Ile Lys Gly Lys Pro Lys Arg Val Val Thr Leu Tyr Gln Gly Ala Thr
25          50          55          60
Asp Val Ala Val Ser Leu Gly Val Lys Pro Val Gly Ala Val Glu Ser
25          65          70          75          80
Trp Thr Gln Lys Pro Lys Phe Glu Tyr Ile Lys Asn Asp Leu Lys Asp
30          85          90          95
Thr Lys Ile Val Gly Gln Glu Pro Ala Pro Asn Leu Glu Glu Ile Ser
30          100          105          110
Lys Leu Lys Pro Asp Leu Ile Val Ala Ser Lys Val Arg Asn Glu Lys
35          115          120          125
Val Tyr Asp Gln Leu Ser Lys Ile Ala Pro Thr Val Ser Thr Asp Thr
35          130          135          140
Val Phe Lys Phe Lys Asp Thr Thr Lys Leu Met Gly Lys Ala Leu Gly
40          145          150          155          160
Lys Glu Lys Glu Ala Glu Asp Leu Leu Lys Lys Tyr Asp Asp Lys Val
40          165          170          175
Ala Ala Phe Gln Lys Asp Ala Lys Ala Lys Tyr Lys Asp Ala Trp Pro
45          180          185          190
Leu Lys Ala Ser Val Val Asn Phe Arg Ala Asp His Thr Arg Ile Tyr
45          195          200          205
Ala Gly Gly Tyr Ala Gly Glu Ile Leu Asn Asp Leu Gly Phe Lys Arg
50          210          215          220
Asn Lys Asp Leu Gln Lys Gln Val Asp Asn Gly Lys Asp Ile Ile Gln
50          225          230          235          240
Leu Thr Ser Lys Glu Ser Ile Pro Leu Met Asn Ala Asp His Ile Phe
55          245          250          255

```

Val Val Lys Ser Asp Pro Asn Ala Lys Asp Ala Ala Leu Val Lys Lys
 260 265 270

5 Thr Glu Ser Glu Trp Thr Ser Ser Lys Glu Trp Lys Asn Leu Asp Ala
 275 280 285

Val Lys Asn Asn Gln Val Ser Asp Asp Leu Asp Glu Ile Thr Trp Asn
 290 295 300

10 Leu Ala Gly Gly Tyr Lys Ser Ser Leu Lys Leu Ile Asp Asp Leu Tyr
 305 310 315 320

Glu Lys Leu Asn Ile Glu Lys Gln Ser Lys
 325 330

(2) INFORMATION FOR SEQ ID NO:5194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5194:

30 Met Thr Arg Lys Phe Arg Thr Leu Ile Leu Ile Ala Thr Ile
 1 5 10 15

Ala Leu Ser Gly Cys Ala Asn Asp Asp Gly Ile Tyr Ser Asp Lys Gly
 20 25 30

35 Gln Val Phe Arg Lys Ile Leu Ser Ser Asp Leu Thr Ser Leu Asp Thr
 35 40 45

Ser Leu Ile Thr Asp Glu Ile Ser Ser Glu Val Thr Ala Gln Thr Phe
 50 55 60

40 Glu Gly Leu Tyr Thr Leu Gly Lys Gly Asp Lys Pro Val Leu Gly Val
 65 70 75 80

Ala Lys Ala Phe Pro Glu Lys Ser Lys Asp Gly Lys Thr Leu Lys Val
 85 90 95

45 Lys Leu Arg Ser Asp Ala Lys Trp Ser Asn Gly Asp Lys Val Thr Ala
 100 105 110

50 Gln Asp Phe Val Tyr Ala Trp Arg Lys Thr Val Asp Pro Lys Thr Gly
 115 120 125

Ser Glu Phe Ala Tyr Ile Met Gly Asp Ile Lys Asn Ala Ser Asp Ile
 130 135 140

55 Ser Thr Gly Lys Lys Pro Val Glu Gln Leu Gly Ile Lys Ala Leu Asn
 145 150 155 160

Asp Glu Thr Leu Gln Ile Glu Leu Glu Lys Pro Val Pro Tyr Ile Asn
 165 170 175
 Gln Leu Leu Ala Leu Asn Thr Phe Ala Pro Gln Asn Glu Lys Val Ala
 180 185 190
 Lys Lys Tyr Gly Lys Asn Tyr Gly Thr Ala Ala Asp Arg Ala Val Tyr
 195 200 205
 Asn Gly Pro Phe Lys Val Asp Asp Trp Lys Gln Glu Asp Lys Thr Leu
 210 215 220
 Leu Ser Lys Asn Gln Tyr Tyr Trp Asp Lys Lys Asn Val Lys Leu Asp
 225 230 235 240
 Lys Val Asn Tyr Lys Val Ile Lys Asp Leu Gln Ala Gly Ala Ser Leu
 245 250 255
 Tyr Asp Thr Glu Ser Val Asp Asp Ala Phe Ile Thr Ala Asp Gln Val
 260 265 270
 Asn Lys Tyr Lys Asp Asn Lys Gly Leu Asn Phe Val Leu Thr Thr Gly
 275 280 285
 Thr Phe Phe Val Lys Met Asn Glu Lys Gln Tyr Pro Asp Phe Lys Asn
 290 295 300
 Lys Asn Leu Arg Leu Xaa Ser His Lys Gln
 305 310

(2) INFORMATION FOR SEQ ID NO:5195:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 280 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5195:

Met Lys Arg Leu Ile Gly Leu Val Ile Val Ala Leu Val Leu Leu Ala
 1 5 10 15
 Ala Cys Gly Gly Asn Asn Asp Lys Lys Val Thr Ile Gly Val Ala Ser
 20 25 30
 Asn Asp Thr Lys Ala Trp Glu Lys Val Lys Glu Leu Ala Lys Lys Asp
 35 40 45
 Asp Ile Asp Val Glu Ile Lys His Phe Ser Asp Tyr Asn Leu Pro Asn
 50 55 60
 Lys Ala Leu Asn Asp Gly Asp Ile Asp Met Asn Ala Phe Gln His Phe
 65 70 75 80

Ala Phe Leu Asp Gln Tyr Lys Lys Ala His Lys Gly Thr Lys Ile Ser
85 90 95

5 Ala Leu Ser Thr Thr Val Leu Ala Pro Leu Gly Ile Tyr Ser Asp Lys
100 105 110

Ile Lys Asp Val Lys Lys Val Lys Asp Gly Ala Lys Val Ile Pro
115 120 125

10 Asn Asp Val Ser Asn Gln Ala Arg Ala Leu Lys Leu Leu Glu Ala Ala
130 135 140

Gly Leu Ile Lys Leu Lys Lys Asp Phe Gly Leu Ala Gly Thr Val Lys
145 150 155 160

15 Asp Ile Thr Ser Asn Pro Lys His Leu Lys Ile Thr Ala Val Asp Ala
165 170 175

Gln Gln Thr Ala Arg Ala Leu Ser Asp Val Asp Ile Ala Val Ile Asn
180 185 190

20 Asn Gly Val Ala Thr Lys Ala Gly Lys Asp Pro Lys Asn Asp Pro Ile
195 200 205

25 Phe Leu Glu Lys Ser Asn Ser Asp Ala Val Lys Pro Tyr Ile Asn Ile
210 215 220

Val Ala Val Asn Asp Lys Asp Leu Asp Asn Lys Thr Tyr Ala Lys Ile
225 230 235 240

30 Val Glu Leu Tyr His Ser Lys Glu Ala Gln Lys Ala Leu Gln Glu Asp
245 250 255

Val Lys Asp Gly Glu Lys Pro Val Asn Leu Ser Lys Asp Glu Ile Lys
260 265 270

35 Ala Ile Glu Thr Ser Leu Ala Lys
275 280

(2) INFORMATION FOR SEQ ID NO:5196:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5196:

Met Lys Lys Leu Phe Gly Leu Ile Leu Val Leu Thr Phe Ala Val Val
1 5 10 15

55 Leu Ala Ala Cys Gly Asn Gly Asn Lys Ser Gly Ser Asp Asp Lys Lys
20 25 30

Ile Thr Val Ser Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys
 35 40 45
 Ala Lys Pro Leu Leu Glu Lys Lys Gly Tyr Glu Leu Asp Ile Lys Thr
 5 50 55 60
 Ile Asn Asp Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile
 65 70 75 80
 Asp Ala Asn Tyr Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Lys Lys
 10 85 90 95
 Asp Lys Gly Tyr Lys Ile Val Ser Ala Gly Asp Val His Leu Glu Pro
 100 105 110
 Met Ala Val Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Glu Leu Pro Lys
 15 115 120 125
 Gly Ala Thr Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe
 130 135 140
 Leu Lys Phe Phe Val Asp Ala Gly Leu Ile Lys Ile Lys Lys Gly Val
 145 150 155 160
 Lys Ile Glu Asp Ala Lys Phe Ser Asp Ile Thr Glu Asn Lys Lys Asp
 25 165 170 175
 Ile Lys Phe Asn Asn Lys Gln Ser Ala Glu Phe Leu Pro Lys Ile Tyr
 180 185
 Gln Asn Glu Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Phe Ala Ile
 30 195 200 205
 Glu Gln Lys Leu Asn Pro Lys Lys Asp Ser Ile Ala Val Glu Ser Ala
 210 215 220
 Lys Asp Asn Pro Tyr Ala Asn Leu Ile Ala Val Lys Glu Gly His Gln
 35 225 230 235 240
 Asp Asp Lys Lys Ile Lys Ala Leu Ile Glu Val Leu Gln Ser Lys Asp
 245 250 255
 Ile Gln Asp Phe Ile Asn Glu Lys Tyr Asn Gly Ala Val Ile Pro Ala
 40 260 265 270
 Lys

45

(2) INFORMATION FOR SEQ ID NO:5197:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 amino acids
 50 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (iii) MOLECULE TYPE: protein

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5197:

Met Lys Lys Ile Lys Tyr Ile Leu Val Val Phe Val Leu Ser Leu Thr
 1 5 10 15
 Val Leu Ser Gly Cys Ser Leu Pro Gly Leu Gly Ser Lys Ser Thr Lys
 20 25 30
 Asn Asp Val Lys Ile Thr Ala Leu Ser Thr Ser Glu Ser Gln Ile Ile
 35 40 45
 Ser His Met Leu Arg Leu Leu Ile Glu His Asp Thr His Gly Lys Ile
 50 55 60
 Lys Pro Thr Leu Val Asn Asn Leu Gly Ser Ser Thr Ile Gln His Asn
 65 70 75 80
 Ala Leu Ile Asn Gly Asp Ala Asn Ile Ser Gly Val Arg Tyr Asn Gly
 85 90 95
 Thr Asp Leu Thr Gly Ala Leu Lys Glu Ala Pro Ile Lys Asn Pro Lys
 100 105 110
 Lys Ala Met Ile Ala Thr Gln Gln Gly Phe Lys Lys Lys Phe Asp Gln
 115 120 125
 Thr Phe Phe Asp Ser Tyr Gly Phe Ala Asn Thr Tyr Ala Phe Met Val
 130 135 140
 Thr Lys Glu Thr Ala Lys Lys Tyr His Leu Glu Thr Val Ser Asp Leu
 145 150 155 160
 Ala Lys His Ser Lys Asp Leu Arg Leu Gly Met Asp Ser Ser Trp Met
 165 170 175
 Asn Arg Lys Gly Asp Gly Tyr Glu Gly Phe Lys Lys Glu Tyr Gly Phe
 180 185 190
 Asp Phe Gly Thr Val Arg Pro Met Gln Ile Gly Leu Val Tyr Asp Ala
 195 200 205
 Leu Asn Ser Glu Lys Leu Asp Val Ala Leu Gly Tyr Ser Thr Asp Gly
 210 215 220
 Arg Ile Ala Ala Tyr Asp Leu Lys Val Leu Lys Asp Asp Lys Gln Phe
 225 230 235 240
 Phe Pro Pro Tyr Ala Ala Ser Ala Val Ala Thr Asn Glu Leu Leu Arg
 245 250 255
 Gln His Pro Glu Leu Lys Thr Thr Ile Asn Lys Leu Thr Gly Lys Ile
 260 265 270
 Ser Thr Ser Glu Met Gln Arg Leu Asn Tyr Glu Ala Asp Gly Lys Gly
 275 280 285
 Lys Glu Pro Ala Val Val Ala Glu Glu Phe Leu Lys Lys His His Tyr
 290 295 300

Phe Asp Lys Gln Lys Gly Gly His Lys
305 310

(2) INFORMATION FOR SEQ ID NO:5198:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 284 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5198:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala
1 5 10 15
Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys
20 25 30
Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr
25 35 40 45
Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu
50 55 60
Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala
30 65 70 75 80
Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala
85 90 95
Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp
35 100 105 110
Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile
115 120 125
Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys
40 130 135 140
Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala
45 145 150 155 160
Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp
165 170 175
Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Ile
50 180 185 190
Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala
195 200 205
Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys
55 210 215 220

Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
 225 230 235 240
 Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
 5 245 250 255
 Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
 260 265 270
 Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
 10 275 280

(2) INFORMATION FOR SEQ ID NO:5199:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 284 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5199:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala
 1 5 10 15
 Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys
 30 20 25 30
 Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr
 35 35 40 45
 Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu
 50 55 60
 Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala
 65 70 75 80
 Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala
 40 85 90 95
 Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp
 100 105 110
 Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile
 45 115 120 125
 Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys
 50 130 135 140
 Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala
 145 150 155 160
 Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp
 55 165 170 175

Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile
 180 185 190
 Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala
 195 200 205
 Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys
 210 215 220
 Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
 225 230 235 240
 Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
 245 250 255
 Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
 260 265 270
 Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
 275 280

(2) INFORMATION FOR SEQ ID NO:5200:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 208 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5200:

Met Lys Phe Lys Ala Ile Val Ala Ile Thr Leu Ser Leu Ser Leu Leu
 1 5 10 15
 Thr Ala Cys Gly Ala Asn Gln His Lys Glu Asn Ser Ser Lys Ser Asn
 20 25 30
 Asp Thr Asn Lys Lys Thr Gln Thr Asp Asn Thr Thr Gln Ser Asn
 35 40 45
 Thr Glu Lys Gln Met Thr Pro Gln Glu Ala Glu Asp Ile Val Arg Asn
 50 55 60
 Asp Tyr Lys Ala Arg Gly Val Asn Glu Tyr Gln Thr Leu Asn Tyr Lys
 65 70 75 80
 Thr Asn Leu Glu Arg Ser Asn Glu His Glu Tyr Tyr Val Glu His Leu
 85 90 95
 Val Arg Asp Ala Val Gly Thr Pro Leu Lys Arg Cys Ala Ile Val Asn
 100 105 110
 Arg His Asn Gly Thr Ile Ile Asn Ile Phe Asp Asp Met Ser Glu Lys
 115 120 125

Asp Lys Glu Glu Phe Glu Ala Phe Lys Lys Arg Ser Pro Lys Tyr Asn
 130 135 140
 Pro Gly Met Asn Asn His Asp Glu Thr Asp Gly Glu Ser Glu Asp Ile
 145 150 155 160
 Gln His His Asp Ile Asp Asn Asn Lys Ala Ile Gln Asn Asp Ile Pro
 165 170 175
 Asp Gln Lys Val Asp Asp Lys Asn Asp Lys Asn Ala Val Asn Lys Glu
 180 185 190
 Glu Lys His Asp Asn Gly Ala Asn Asn Ser Glu Glu Thr Lys Val Lys
 195 200 205

(2) INFORMATION FOR SEQ ID NO:5201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5201:

Met Leu Lys Gly Cys Gly Gly Cys Leu Ile Ser Phe Ile Leu Leu Ile
 1 5 10 15
 Ile Leu Leu Ser Ala Cys Ser Met Met Phe Ser Asn Asn Asp Asn Ser
 20 25 30
 Thr Asn Asn Gln Ser Ser Lys Thr Gln Leu Thr Gln Lys Asp Glu Asn
 35 40 45
 Lys Asn Glu Asp Lys Pro Glu Glu Lys Ser Glu Thr Ala Thr Asp Glu
 50 55 60
 Asp Leu Gln Ser Thr Glu Glu Val Pro Ala Asn Glu Asn Thr Glu Asn
 65 70 75 80
 Asn Gln His Glu Ile Asp Glu Ile Thr Thr Lys Asp Gln Ser Asp Asp
 85 90 95
 Asp Ile Asn Thr Pro Asn Val Ala Glu Asp Lys Ser Gln Asp Asp Leu
 100 105 110
 Lys Asp Asp Leu Lys Glu Lys Gln Gln Ser Ser Asn His His Gln Ser
 115 120 125
 Thr Gln Pro Lys Thr Ser Pro Ser Thr Glu Thr Asn Thr Gln Gln Ser
 130 135 140
 Phe Ala Asn Cys Lys Gln Leu Arg Gln Val Tyr Pro Asn Gly Val Thr

Ala Asp His Pro Ala Tyr Arg Pro His Leu Asp Arg Asp Lys Asp Lys
 165 170 175

Arg Ala Cys Glu Pro Asp Lys Tyr
 180

(2) INFORMATION FOR SEQ ID NO:5202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5202:

Met Lys Lys Arg Leu Leu Leu Ser Thr Phe Leu Ala Ser Thr Leu Ile
 1 5 10 15

Leu Thr Gly Cys Ala Ser Asp Gln Ser Asp Asn Glu Asp His His Thr
 20 25 30

Ser Thr Gly Ile His Ala Pro Lys Ser Ala Lys Lys Leu Glu Thr Lys
 35 40 45

Asp Ile Phe Xaa Ser Asp Lys Lys Asn Ser Asp Ile Ser Asp Ala Glu
 50 55 60

Met Lys Gln Ala Ile Glu Lys Tyr Leu Ser Val Asn Ser Asp Ile Leu
 65 70 75 80

Asp Asn Lys Tyr Ile Met Gln His Lys Leu Asp Lys Gln Ile Asp Ser
 85 90 95

Gln Thr Lys Val Thr Glu Lys Gln Ala Glu Thr Leu Ser His Leu Ser
 100 105 110

Asn Leu Ala Val Lys Asn Asp Leu His Phe Lys Lys Phe Val Thr Glu
 115 120 125

Asn Asn Ile Pro Lys Glu Tyr Lys Lys Pro Val Glu Leu Met Met Asn
 130 135 140

Tyr Phe Lys Ala Leu Asn Ser Thr Ile Ala Asn Val Asp Glu Asp Ile
 145 150 155 160

Glu Lys Leu Ser Tyr Gln Pro Gln Asn Lys Ile Asn Val Val Asp Val
 165 170 175

Pro Thr Lys Tyr Ala Gly Asp Val Asn Lys Lys Gln Gln Asp Lys Ile
 180 185 190

Lys Asp Phe Leu Lys Ser Lys Gly Ile Lys Ser Asp Val Ile Asp Lys

(2) INFORMATION FOR SEQ ID NO:5203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5203:

```

Met Lys Ser Lys Ile Tyr Ile Leu Leu Xaa Leu Ile Phe Leu Ser
 1           5           10
Ala Cys Ala Asn Thr Arg His Ser Glu Ser Asp Lys Asn Val Leu Thr
20          20          25          30
Val Tyr Ser Pro Tyr Gln Ser Asn Leu Ile Arg Pro Ile Leu Asn Glu
35          35          40          45
Xaa Glu Lys Gln Glu His Val Lys Ile Glu Ile Lys His Gly Ser Thr
25          50          55          60
Gln Val Leu Leu Ser Asn Leu His Asn Glu Asp Phe Ser Glu Arg Gly
65          70          75          80
Asp Val Phe Met Gly Gly Val Leu Ser Glu Thr Ile Asp His Pro Glu
30          85          90          95
Asp Phe Val Pro Tyr Gln Asp Thr Ser Val Thr Gln Gln Leu Glu Asp
35          100         105         110
Tyr Arg Ser Asn Asn Lys Tyr Val Thr Ser Phe Leu Leu Met Pro Thr
115         120         125
Val Ile Val Val Asn Ser Asp Leu Gln Gly Asp Ile Lys Ile Arg Gly
40          130         135         140
Tyr Gln Asp Leu Leu Gln Pro Ile Leu Lys Gly Lys Ile Ala Tyr Ser
145         150         155         160
Asn Pro Asn Thr Thr Thr Thr Gly Tyr Gln His Met Arg Ala Ile Tyr
45          165         170         175
Ser Met His His Arg Val Ser Asp Val His Gln Phe Gln Asn His Ala
180         185         190
Met Gln Leu Ser Lys Thr Ser Lys Val Ile Glu Asp Val Ala Lys Gly
50          195         200         205
Lys Tyr Tyr Ala Gly Leu Ser Tyr Glu Gln Asp Ala Arg Thr Trp Lys
210         215         220

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225 230 235 240
 Leu Asn Val Asp Gly Ile Ala Leu Val Lys Asn Ala His Pro His Pro
 245 250 255
 5 Lys Arg Lys Lys Leu Val Gln Tyr Leu Thr Ser Arg Ser Val Gln Gln
 260 265 270
 Arg Leu Val Ala Glu Phe Asp Ala Lys Ser Ile
 275 280
 10

(2) INFORMATION FOR SEQ ID NO:5204:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 309 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5204:
 25 Met Lys Lys Phe Ile Gly Ser Val Leu Ala Thr Thr Leu Ile Leu Gly
 1 5 10 15
 Gly Cys Ser Thr Met Glu Asn Glu Ser Lys Lys Asp Thr Lys Thr Glu
 20 25 30
 30 Thr Lys Ser Val Pro Glu Glu Met Glu Ala Ser Lys Tyr Val Gly Gln
 35 40 45
 Gly Phe Gln Pro Pro Ala Glu Lys Asn Ala Ile Glu Phe Ala Lys Lys
 50 55 60
 35 His Arg Lys Glu Phe Glu Lys Val Gly Glu Gln Phe Phe Lys Asp Asn
 65 70 75 80
 Phe Gly Leu Lys Val Lys Ala Thr Asn Val Val Gly Lys Asp Asp Gly
 85 90 95
 40 Val Glu Val Tyr Val His Cys Glu Asp His Gly Ile Val Phe Asn Ala
 100 105 110
 45 Ser Leu Pro Leu Tyr Lys Asp Ala Ile His Gln Lys Gly Ser Met Arg
 115 120 125
 Ser Asn Asp Asn Gly Asp Asp Met Ser Met Met Val Gly Thr Val Leu
 130 135 140
 50 Ser Gly Phe Glu Tyr Arg Ala Gln Lys Glu Lys Tyr Asp Asn Leu Tyr
 145 150 155 160
 Lys Phe Phe Lys Glu Asn Glu Lys Lys Tyr Gln Tyr Thr Gly Phe Thr
 165 170 175
 55

180 185 190
 Phe Tyr Ile Thr Tyr Ser Ser Arg Ser Leu Lys Glu Tyr Arg Lys Tyr
 195 200 205
 Tyr Glu Pro Leu Ile Arg Lys Asn Asp Lys Glu Phe Lys Glu Gly Met
 210 215 220
 Glu Arg Ala Arg Lys Glu Val Asn Tyr Ala Ala Asn Thr Asp Ala Val
 225 230 235 240
 Ala Thr Leu Phe Ser Thr Lys Lys Asn Phe Thr Lys Asp Asn Thr Val
 245 250 255
 Asp Asp Val Ile Glu Leu Ser Asp Lys Leu Tyr Asn Leu Lys Asn Lys
 260 265 270
 Pro Asp Lys Ser Thr Ile Thr Ile Gln Ile Gly Lys Pro Thr Ile Asn
 275 280 285
 Thr Lys Lys Ala Phe Tyr Asp Asp Asn Arg Pro Ile Glu Tyr Gly Val
 290 295 300
 His Ser Lys Asp Glu
 305

(2) INFORMATION FOR SEQ ID NO:5205:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5205:

Met Lys Lys Leu Val Ser Ile Val Gly Ala Thr Leu Leu Leu Ala Gly
 1 5 10 15
 Cys Gly Ser Gln Asn Leu Ala Pro Leu Glu Glu Lys Thr Thr Asp Leu
 20 25 30
 Arg Glu Asp Asn His Gln Leu Lys Leu Asp Ile Gln Glu Leu Asn Gln
 35 40 45
 Gln Ile Ser Asp Ser Lys Ser Lys Ile Lys Gly Leu Glu Lys Asp Lys
 50 55 60
 Glu Asn Ser Lys Lys Thr Ala Ser Asn Asn Thr Lys Ile Lys Leu Met
 65 70 75 80
 Asn Val Thr Ser Thr Tyr Tyr Asp Lys Val Ala Lys Ala Leu Lys Ser
 85 90 95

100 105 110
 Val Gln Ser Lys Leu Asn Gln Ile Ser Asn Asp Ile Gln Ser Ala His
 115 120 125
 5 Thr Ser Tyr Lys Asp Ala Ile Asp Gly Leu Ser Leu Ser Asp Asp Asp
 130 135 140
 Lys Lys Thr Ser Lys Asn Ile Asp Lys Leu Asn Ser Asp Leu Asn His
 145 150 155 160
 10 Ala Phe Asp Asp Ile Lys Asn Gly Tyr Gln Asn Lys Asp Lys Lys Gln
 165 170 175
 Leu Thr Lys Gly Gln Gln Ala Leu Ser Lys Leu Asn Leu Asn Ala Lys
 180 185 190
 15 Ser

(2) INFORMATION FOR SEQ ID NO:5206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 25
 (ii) MOLECULE TYPE: protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5206:

35 Met Lys Arg Leu Leu Phe Val Met Ile Ala Phe Val Phe Ile Leu Ala
 1 5 10 15
 Ala Cys Gly Asn Asn Ser Ser Lys Asp Lys Glu Ala Ser Lys Asp Ser
 20 25 30
 40 Lys Thr Ile Asn Val Gly Thr Glu Gly Thr Tyr Ala Pro Phe Ser Phe
 35 40 45
 His Asp Lys Asp Gly Lys Leu Thr Gly Tyr Asp Ile Asp Val Ile Lys
 50 55 60
 45 Ala Val Ala Lys Glu Glu Gly Leu Lys Leu Lys Phe Asn Glu Thr Ser
 65 70 75 80
 Trp Asp Ser Met Phe Ala Gly Leu Asp Ala Gly Arg Phe Asp Val Ile
 85 90 95
 50 Ala Asn Gln Val Gly Ile Asn Pro Asp Arg Glu Lys Lys Tyr Lys Phe
 100 105 110
 Ser Lys Pro Tyr Thr Phe Ser Ser Ala Val Leu Val Ile Arg Glu Asn
 115 120 125
 55

130 135 140
 Gln Thr Phe Thr Ser Asn Tyr Gly Lys Leu Ala Lys Asp Lys Gly Ala
 145 150 155 160
 5 Asp Ile Thr Lys Val Asp Gly Phe Asn Gln Ser Met Asp Leu Leu Leu
 165 170 175
 Ser Lys Arg Val Asp Gly Thr Phe Asn Asp Ser Leu Ser Tyr Leu Asp
 10 180 185 190
 Tyr Lys Lys Gln Lys Pro Asn Ala Lys Ile Lys Ala Ile Lys Gly Asn
 195 200 205
 15 Ala Glu Gln Ser Arg Ser Ala Phe Ala Phe Ser Lys Lys Ala Asp Asp
 210 215 220
 Glu Thr Val Gln Lys Phe Asn Asp Gly Leu Lys Lys Ile Glu Glu Asn
 225 230 235 240
 20 Gly Glu Leu Ala Lys Ile Gly Lys Lys Trp Phe Gly Gln Asp Val Ser
 245 250 255
 Lys Ser Lys

25 (2) INFORMATION FOR SEQ ID NO:5207:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 amino acids
 (B) TYPE: amino acid
 30 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5207:

40 Met Gly Val His Ser Met Lys Leu Lys Arg Leu Phe Ala Val Val Ile
 1 5 10 15
 Ala Met Leu Leu Val Leu Ala Gly Cys Ser Asn Ser Asn Asp Asn Asn
 20 25 30
 45 Glu Ser Lys Lys Asp Asp Ala Asp Asn Gly Lys Lys Gln Glu Ile Gln
 35 40 45
 Val Ala Ala Ala Ala Ser Leu Thr Asp Val Thr Lys Lys Leu Ala Ser
 50 55 60
 50 Glu Phe Lys Lys Glu His Lys Asn Ala Asp Ile Lys Phe Asn Tyr Gly
 65 70 75 80
 Gly Ser Gly Ala Leu Arg Lys Gln Ile Glu Ser Gly Ala Pro Val Asp
 85 90 95

100 105 110
 Asn Lys Ala His Asp Thr Tyr Lys Tyr Ala Lys Asn Ser Leu Val Leu
 115 120 125
 5 Ile Gly Asp Lys Asp Ser Asn Tyr Thr Ser Val Lys Asp Leu Lys Asp
 130 135 140
 Asn Asp Lys Leu Ala Leu Gly Glu Val Lys Thr Val Ser Ala Gly Lys
 145 150 155 160
 10 Tyr Ala Lys Gln Tyr Leu Asp Asn Asn Asn Leu Phe Lys Glu Val Glu
 165 170 175
 Ser Xaa Ile Val Tyr Ala Lys Asp Val Lys Gln Val Leu Asn Tyr Val
 180 185 190
 15 Xaa Lys Gly Asn Ala Lys Gln Gly Phe Val Tyr
 195 200

(2) INFORMATION FOR SEQ ID NO:5208:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5208:

Met Lys Lys Trp Gln Phe Val Gly Thr Thr Ala Leu Gly Ala Thr Leu
 1 5 10 15
 35 Leu Leu Gly Ala Cys Gly Gly Gly Asn Gly Gly Ser Gly Asn Ser Asp
 20 25 30
 40 Leu Lys Gly Glu Ala Lys Gly Asp Gly Ser Ser Thr Val Ala Pro Ile
 35 40 45
 Val Glu Lys Leu Asn Glu Lys Trp Ala Gln Asp His Ser Asp Ala Lys
 50 55 60
 45 Ile Ser Ala Gly Gln Ala Gly Thr Gly Ala Gly Phe Gln Lys Phe Ile
 65 70 75 80
 Ala Gly Asp Ile Asp Phe Ala Asp Ala Ser Arg Pro Ile Lys Asp Glu
 85 90 95
 50 Glu Lys Gln Lys Leu Gln Asp Lys Asn Ile Lys Tyr Lys Glu Phe Lys
 100 105 110
 Ile Ala Gln Asp Gly Val Thr Val Ala Val Asn Lys Glu Asn Asp Phe
 115 120 125

55

130 135 140
 Ala Lys Thr Trp Lys Asp Val Asn Ser Lys Trp Pro Asp Lys Lys Ile
 145 150 155 160
 5 Asn Ala Val Ser Pro Asn Ser Ser His Gly Thr Tyr Asp Phe Phe Glu
 165 170 175
 Asn Glu Val Met Asn Lys Glu Asp Ile Lys Ala Glu Lys Asn Ala Asp
 180 190
 10 Thr Asn Ala Ile Val Ser Ser Val Thr Lys Asn Lys Glu Gly Ile Gly
 195 200 205
 Tyr Phe Gly Tyr Asn Phe Tyr Val Gln Asn Lys Asp Lys Leu Lys Glu
 210 215 220
 15 Val Lys Ile Lys Asp Glu Asn Gly Lys Ala Thr Glu Pro Thr Lys Lys
 225 230 235 240
 Thr Ile Gln Asp Asn Ser Tyr Ala Leu Ser Arg Pro Leu Phe Ile Tyr
 245 250 255
 Val Asn Glu Lys Ala Leu Lys Asp Asn Lys Val Met Ser Glu Phe Ile
 260 265 270
 20 Lys Phe Val Leu Glu Asp Lys Gly Lys Ala Ala Glu Glu Ala Gly Tyr
 275 280 285
 Val Ala Ala Pro Glu Lys Thr Tyr Lys Ser Gln Leu Asp Asp Leu Lys
 290 295 300
 30 Ala Phe Ile Asp Lys Asn Gln Lys Ser Asp Asp Lys Lys Ser Asp Asp
 305 310 315 320
 Lys Lys Ser Glu Asp Lys Lys
 325
 35

(2) INFORMATION FOR SEQ ID NO:5209:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5209:

Met Lys Arg Leu Ser Ile Ile Val Ile Ile Gly Ile Phe Ile Ile Thr
 1 5 10 15
 Gly Cys Asp Trp Gln Arg Thr Ser Lys Glu Arg Ser Lys Asn Ala Gln
 20 25 30

	35	40	45
5	Asn Leu Met Met Thr Lys 50	Lys Leu Leu Ser Gln Tyr 55	Asn His Pro Lys 60
	Tyr Lys Leu Glu Leu Val Lys 65	Phe Asn Asn Trp 70	Pro Asp Leu Met Asp 75 80
10	Ala Leu Asn Ser Gly Arg Ile 85	Asp Gly Ala Ser Thr 90	Leu Ile Glu Leu 95
	Ala Met Lys Ser Lys Gln Lys 100	Gly Ser Asn Ile Lys 105	Ala Val Ala Leu 110
15	Gly His His Glu Gly Asn Val 115	Ile Met Gly Gln Lys 120	Gly Met His Leu 125
	Asn Glu Phe Asn Asn Asn Gly 130	Asp Asp Tyr His Phe 135	Gly Ile Pro His 140
20	Arg Tyr Ser Thr His Tyr 145	Leu Leu Leu Glu Glu Leu Arg 150	Lys Gln Leu 155 160
	Lys Ile Lys Pro Gly His Phe 165	Ser Tyr His Glu Met Ser 170	Pro Ala Glu 175
25	Met Pro Ala Ala Leu Ser Glu 180	His Arg Ile Thr Gly Tyr 185	Ser Val Ala 190
	Glu Pro Phe Gly Ala Leu Gly 195	Glu Lys Leu Gly Lys 200	Gly Lys Thr Leu 205
30	Lys His Gly Asp Asp Val Ile 210	Pro Asp Ala Tyr Cys 215	Cys Val Leu Val 220
	Leu Arg Gly Glu Leu Leu Asp 225	Gln His Lys Asp Val Ala 230	Gln Ala Phe 235 240
35	Val Gln Asp Tyr Lys Lys Ser 245	Gly Phe Lys Met Asn Asp 250	Arg Lys Gln 255
	Ser Val Asp Ile Met Thr His 260	His Phe Lys Gln Ser Arg 265	Asp Val Leu 270
40	Thr Gln Ser Ala Ala Trp Thr 275	Ser Tyr Gly Asp Leu Thr 280	Ile Lys Pro 285
45	Ser Gly Tyr Gln Glu Ile Thr 290	Thr Thr Leu Val Lys 295	Gln His His Leu Phe 300
	Asn Pro Pro Ala Tyr Asp 305	Phe Val Glu Pro Ser Leu 310	Tyr Lys Glu 315 320
50	Ala Ser Arg Ser		

(2) INFORMATION FOR SEQ ID NO:5210:

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5210:

```

Met Lys Lys Thr Leu Gly Cys Leu Leu Leu Ile Met Leu Leu Val Val
 1             5             10             15

Ala Gly Cys Ser Phe Gly Gly Asn His Lys Leu Ser Ser Lys Lys Ser
15             20             25             30

Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Glu Lys
35             40             45

Asp Pro Asp Leu Glu Lys Tyr Glu Glu Ile Glu Lys Lys Met Lys Gly
20             50             55             60

Ile Lys Asp Ala Pro Ser Leu Asp Lys Leu Asp Pro Leu Met Thr Glu
65             70             75             80

Lys Ser Phe Thr Asn Ser Lys Gly Ile Gln Gly Trp Lys Asp Tyr Lys
25             85             90             95

Glu Leu Met Gly Lys Val Glu Leu Ala Asp Tyr Arg Phe Thr Lys Asp
30             100            105            110

Ser Lys Gly Ser Ser Ile Lys Asp Val Asp Ala Phe Phe Lys Gly Lys
115            120            125

Lys Gly Ile Lys Arg Lys Val Ile Glu Thr His Asp Asp Val Lys Gln
35             130            135            140

Val Asp Tyr Trp
145

```

(2) INFORMATION FOR SEQ ID NO:5211:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5211:

```

Trp Pro Cys Ala Thr Xaa Gln Glx Glu Trp Trp Ser Arg His Xaa Trp
1             5             10             15

```

20

25

30

His

5

(2) INFORMATION FOR SEQ ID NO:5212:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 490 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5212:

20

Met Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr Lys
 1 5 10 15

Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn
 20 25 30

25

Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly
 35 40 45

Trp Lys Val Leu Phe Gly Leu Leu Lys Gly Leu Gly Ala Lys Asp
 50 55 60

30

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
 65 70 75 80

Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
 85 90 95

35

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
 100 105 110

Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Trp
 115 120 125

40

Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
 130 135 140

Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe
 145 150 155 160

45

Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr Gln Ala Pro
 165 170 175

Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile
 180 185 190

50

Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Ser Asn
 195 200 205

55

	210	215	220
	Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Leu Ser Arg Leu		
	225	230	235 240
5	Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp Gln		
		245	250 255
	Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile Gly		
10		260	265 270
	Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala Asp		
		275	280 285
	Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys Ala		
15		290	295 300
	Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile Arg		
		305	310 315
	Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser Val		
20		325	330 335
	Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu Asp		
		340	345 350
	Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala Tyr		
25		355	360 365
	Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser Ala		
		370	375 380
	Ser Ser Asn Thr Val Lys Pro Val Ala Ser Ala Trp Lys Arg Asn Lys		
30		385	390 395
	Tyr Gly Thr Tyr Tyr Met Glu Glu Ser Ala Arg Phe Thr Asn Gly Asn		
		405	410 415
35	Gln Pro Ile Thr Val Arg Lys Val Gly Pro Phe Leu Ser Cys Pro Val		
		420	425 430
	Gly Tyr Gln Phe Gln Pro Gly Gly Tyr Cys Asp Tyr Thr Glu Val Met		
40		435	440 445
	Leu Gln Asp Gly His Val Trp Val Gly Tyr Thr Trp Glu Gly Gln Arg		
		450	455 460
	Tyr Tyr Leu Pro Ile Arg Thr Trp Asn Gly Ser Ala Pro Pro Asn Gln		
45		465	470 475
	Ile Leu Gly Asp Leu Trp Gly Glu Ile Ser		
		485	490

50 (2) INFORMATION FOR SEQ ID NO:5213:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 299 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

55

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5213:

Gly Asp Lys Met Asn Lys Ile Ser Lys Tyr Ile Ala Ile Ala Ser Leu
 1 5 10 15
 Ser Val Ala Val Thr Val Ser Ala Pro Gln Thr Thr Asn Ser Thr Ala
 20 25 30
 Phe Ala Lys Ser Ser Ala Glu Val Gln Gln Thr Gln Gln Ala Ser Ile
 35 40 45
 Pro Ala Ser Gln Lys Ala Asn Leu Gly Asn Gln Asn Ile Met Ala Val
 50 55 60
 Ala Trp Tyr Gln Asn Ser Ala Glu Ala Lys Ala Leu Tyr Leu Gln Gly
 65 70 75 80
 Tyr Asn Ser Ala Lys Thr Gln Leu Asp Lys Glu Ile Lys Lys Asn Lys
 85 90 95
 Gly Lys His Lys Leu Ala Ile Ala Leu Asp Leu Asp Glu Thr Val Leu
 100 105 110
 Asp Asn Ser Pro Tyr Gln Gly Tyr Ala Ser Ile His Asn Lys Pro Phe
 115 120 125
 Pro Glu Gly Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val
 130 135 140
 Tyr Gly Ala Lys Glu Phe Leu Lys Tyr Ala Asp Lys Lys Gly Val Asp
 145 150 155 160
 Ile Tyr Tyr Ile Ser Asp Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr
 165 170 175
 Gln Lys Asn Leu Lys Gln Gln Gly Ile Pro Gln Ala Lys Lys Ser His
 180 185 190
 Ile Leu Leu Lys Gly Lys Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln
 195 200 205
 Met Val Gln Lys Asp His Lys Leu Val Met Leu Phe Gly Asp Asn Leu
 210 215 220
 Leu Asp Phe Thr Asp Pro Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala
 225 230 235 240
 Leu Ile Glu Lys His Lys Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe
 245 250 255
 Pro Asn Pro Met Tyr Gly Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn
 260 265 270

275

280

285

Lys Gln Phe Asp Pro Lys Thr Gly Glu Val Lys
 290 295

(2) INFORMATION FOR SEQ ID NO:5214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5214:

Leu Asn Lys Cys Lys Ile Ile Ile Trp Arg Ile Ile Asn Met Lys Asn
 1 5 10 15
 Lys Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile Gly Ile Thr
 20 25 30
 Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro
 35 40 45
 Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn
 50 55 60
 Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro
 65 70 75 80
 Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp
 85 90 95
 Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala
 100 105 110
 Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln
 115 120 125
 Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg
 130 135 140
 Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys
 145 150 155 160
 Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu
 165 170 175
 Val Lys

(2) INFORMATION FOR SEQ ID NO:5215:

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5215:

Lys Glu Arg Val Leu Met Lys Lys Leu Thr Ala Ser Ile Ile Ala
 1 5 10 15
 15 Cys Ser Val Val Met Gly Val Gly Leu Val Asn Thr Ser Ala Glu Ala
 20 25 30
 Ala Ser Gly Asn Ser Ile Asp Thr Val Lys Gln Leu Ile Lys Gly Asp
 35 40 45
 20 Gln Ser Leu Glu Asn Val Lys Ile Gly Glu Ser Ile Lys Asp Val Leu
 50 55 60
 Thr Lys Tyr Lys Asn Pro Met Tyr Ser Tyr Asn Glu Asp Gly Thr Glu
 65 70 75 80
 25 His Tyr Tyr Glu Phe His Thr Lys Lys Gly Met Leu Leu Val Thr Thr
 85 90 95
 Asp Gly Lys Lys Asn Asn Gly Lys Val Thr His Ile Ser Met Met Tyr
 100 105 110
 30 Asn Asp Ala Asn Gly Pro Thr Tyr Gln Ala Val Lys Asn Tyr Val Gly
 115 120 125
 35 Lys Ala Val Thr His Thr Glu Tyr Ser Lys Val Ala Gly Asn Phe Gly
 130 135 140
 Tyr Ile Glu Lys Gly Lys Thr Thr Tyr Gln Phe Ala Ser Ala Pro Lys
 145 150 155 160
 40 Asp Lys Asn Ile Lys Leu Tyr Arg Ile Asp Leu Glu Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:5216:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5216:

1 5 10 15
 Asn Glu Asp Gly Ser Lys Lys Lys Met Ser Thr Thr Ala Lys Val Val
 20 25 30
 5 Ser Ile Ala Thr Val Leu Leu Leu Leu Gly Gly Leu Val Phe Ala Ile
 35 40 45
 Phe Ala Tyr Val Asp His Ser Asn Lys Ala Lys Glu Arg Met Leu Asn
 50 55 60
 10 Glu Gln Lys Gln Gln Lys Lys Glu Lys Arg Gln Lys Glu Asn Ala Glu
 65 70 75 80
 15 Lys Glu Arg Lys Lys Lys Gln Gln Glu Glu Lys Glu Gln Asn Glu Leu
 85 90 95
 Asp Ser Gln Ala Asn Gln Tyr Gln Gln Leu Pro Gln Gln Asn Gln Tyr
 100 105 110
 20 Gln Tyr Val Pro Pro Gln Gln Gln Ala Pro Thr Lys Gln Arg Pro Ala
 115 120 125
 Lys Glu Glu Asn Asp Asp Lys Ala Ser Lys Asp Glu Ser Lys Asp Lys
 130 135 140
 25 Asp Asp Lys Ala Ser Gln Asp Lys Ser Asp Asp Asn Gln Lys Lys Thr
 145 150 155 160
 Asp Asp Asn Lys Gln Pro Ala
 165
 30

(2) INFORMATION FOR SEQ ID NO:5217:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 35

(ii) MOLECULE TYPE: protein
 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5217:
 45

Met Lys Arg Asn Phe Pro Lys Leu Ile Ala Leu Ser Leu Ile Phe Ser
 1 5 10 15
 Leu Ser Val Thr Thr Pro Ile Ala Asn Ala Glu Ser Asn Ser Asn Ile Lys
 20 25 30
 Ala Lys Asp Lys Lys His Val Gln Val Asn Val Glu Asp Lys Ser Val
 35 40 45
 55 Pro Thr Asp Val Arg Asn Leu Ala Gln Lys Asp Tyr Leu Ser Tyr Val
 50 55 60

65 70 75 80
Gly Glu Pro Phe Lys Ile Tyr Lys Phe Asn Lys Lys Ser Asp Gly Asn
 85 90 95
Tyr Tyr Phe Pro Val Leu Asn Thr Glu Gly Asn Ile Asp Tyr Ile Val
 100 105 110
Thr Ile Ser
 115

(2) INFORMATION FOR SEO ID NO:5218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5218:

	Asn	Phe	Lys	Met	Gln	Glu	Val	Lys	Tyr	Met	Thr	Glu	Ile	Thr	Phe	Lys
	1			5						10					15	
30	Gly	Gly	Pro	Ile	His	Leu	Lys	Gly	Gln	Gln	Ile	Asn	Glu	Gly	Asp	Phe
			20						25					30		
	Ala	Pro	Asp	Phe	Thr	Val	Leu	Asp	Asn	Asp	Leu	Asn	Gln	Val	Thr	Leu
		35						40					45			
35	Ala	Asp	Tyr	Ala	Gly	Lys	Lys	Lys	Leu	Ile	Ser	Val	Val	Pro	Ser	Ile
	50					55						60				
	Asp	Thr	Gly	Val	Cys	Asp	Gln	Gln	Thr	Arg	Lys	Phe	Asn	Ser	Asp	Ala
	65				70					75						80
40	Ser	Lys	Glu	Glu	Gly	Ile	Val	Leu	Thr	Ile	Ser	Ala	Asp	Leu	Pro	Phe
					85					90					95	
	Ala	Gln	Lys	Arg	Trp	Cys	Ala	Ser	Ala	Gly	Leu	Asp	Asn	Val	Ile	Thr
			100					105						110		
45	Leu	Ser	Asp	His	Arg	Asp	Leu	Ser	Phe	Gly	Glu	Asn	Tyr	Gly	Val	Val
			115					120					125			
	Met	Glu	Glu	Leu	Arg	Leu	Leu	Ala	Arg	Ala	Val	Phe	Val	Leu	Asp	Ala
50		130				135						140				
	Asp	Asn	Lys	Val	Val	Tyr	Lys	Glu	Ile	Val	Ser	Glu	Gly	Thr	Asp	Phe
	145				150						155					160
55	Pro	Asp	Phe	Asp	Ala	Ala	Leu	Ala	Ala	Tyr	Lys	Asn	Ile			
				165					170							

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5219:

```

15   Ile Glu Ser Arg Phe Ile Met Ala Lys Ile Asn Phe Asp Ala Ala Thr
      1             5             10             15

      Lys Gly Asn Pro Gly Ile Ser Thr Cys Ala Ile Val Ile Lys Glu Asp
            20             25             30

20   Glu Gln His Tyr Thr Thr His Glu Leu Gly Glu Met Asp Asn His
      35             40             45

      Thr Ala Glu Trp Ala Ala Cys Ile Tyr Ala Leu Glu His Ala Arg Glu
            50             55             60

25   Leu Asn Val Gln Asn Ala Leu Leu Tyr Thr Asp Ser Lys Leu Ile Ala
      65             70             75             80

      Asp Ser Ile Glu Ala Gly Tyr Val Lys Asn Ala Asn Phe Lys Pro Tyr
            85             90             95

30   Phe Asp Gln Ile Glu Ile Phe Glu Lys Asp Phe Asp Leu Leu Phe Val
      100            105            110

      Lys Trp Ile Pro Arg Glu Gln Asn Lys Glu Ala Asn Gln His Ala Gln
            115            120            125

35   Gln Ala Leu Tyr Lys Leu Ile Lys Lys Asn Lys
      130            135

```

(2) INFORMATION FOR SEQ ID NO:5220:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5220:

```

55   Met Pro Gly Thr Val Leu Asp Pro Gln Met Ile Lys Asn Glu Asp Val
      1             5             10             15

```

[illegible]

(2) INFORMATION FOR SEQ ID NO:5221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5221:

		Ile	Met	Ala	Tyr	Asp	Gly	Leu	Phe	Thr	Lys	Lys	Met	Val	Glu	Ser	Leu
	1					5					10					15	
45		Gln	Phe	Leu	Thr	Thr	Gly	Arg	Val	His	Lys	Ile	Asn	Gln	Pro	Asp	Asn
					20					25					30		
		Asp	Thr	Ile	Leu	Met	Val	Val	Arg	Gln	Asn	Arg	Gln	Asn	His	Gln	Leu
					35				40					45			
50		Leu	Leu	Ser	Ile	His	Pro	Asn	Phe	Ser	Arg	Leu	Gln	Leu	Thr	Thr	Lys
					50			55					60				
		Lys	Tyr	Asp	Asn	Pro	Phe	Asn	Pro	Pro	Met	Phe	Ala	Arg	Val	Phe	Arg
		65				70						75				80	

	85	90	95
	Asp Arg Arg Ile Glu Ile Asp Ile Lys Ser Lys Asp Glu Ile Gly Asp		
	100	105	110
5	Thr Ile Tyr Arg Thr Val Ile Leu Glu Ile Met Gly Lys His Ser Asn		
	115	120	125
	Leu Ile Leu Val Asp Glu Asn Arg Lys Ile Ile Glu Gly Phe Lys His		
10	130	135	140
	Leu Thr Pro Asn Thr Asn His Tyr Arg Thr Val Met Pro Gly Phe Asn		
	145	150	155
	Tyr Glu Ala Pro Pro Thr Gln His Lys Ile Asn Pro Tyr Asp Ile Thr		
15	165	170	175
	Gly Ala Glu Val Leu Lys Tyr Ile Asp Phe Asn Ala Gly Asn Ile Ala		
	180	185	190
20	Lys Gln Leu Leu Asn Gln Phe Glu Gly Phe Ser Pro Leu Ile Thr Asn		
	195	200	205
	Glu Ile Val Ser Arg Arg Gln Phe Met Thr Ser Ser Thr Leu Pro Glu		
	210	215	220
25	Ala Phe Asp Glu Val Met Ala Glu Thr Lys Leu Pro Pro Thr Pro Ile		
	225	230	235
	Phe His Lys Asn His Glu Thr Gly Lys Glu Asp Phe Tyr Phe Ile Lys		
30	245	250	255
	Leu Asn Gln Phe Asn Asp Asp Thr Val Thr Tyr Asp Ser Leu Asn Asp		
	260	265	270
35	Leu Leu Asp Arg Phe Tyr Asp Ala Arg Gly Glu Arg Glu Arg Val Lys		
	275	280	285
	Gln Arg Ala Asn Asp Leu Val Arg Phe Val Gln Gln Gln Leu His Lys		
	290	295	300
40	Tyr Gln Asn Lys Leu Ala Ser		
	305	310	

(2) INFORMATION FOR SEQ ID NO:5222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 245 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5222:

	1		5		10		15									
	Glu	Gln	Leu	Tyr	Gly	Glu	Leu	Ile	Thr	Ala	Asn	Ile	Tyr	Arg	Ile	Lys
				20					25					30		
5	Gln	Gly	Asp	Lys	Glu	Val	Thr	Ala	Leu	Asn	Tyr	Tyr	Thr	Asn	Glu	Glu
		35						40					45			
10	Val	Val	Ile	Pro	Leu	Asn	Pro	Thr	Lys	Ser	Pro	Ser	Ala	Asn	Ala	Gln
		50					55					60				
	Tyr	Tyr	Tyr	Lys	Gln	Tyr	Xaa	Arg	Met	Lys	Thr	Arg	Xaa	Arg	Glu	Leu
	65				70					75					80	
15	Gln	His	Gln	Ile	Gln	Leu	Thr	Lys	Asp	Asn	Ile	Asp	Tyr	Phe	Ser	Thr
					85					90					95	
	Ile	Glu	Gln	Gln	Leu	His	His	Ile	Ser	Val	His	Asp	Ile	Asp	Glu	Ile
				100					105					110		
20	Arg	Asp	Glu	Leu	Ala	Glu	Gln	Gly	Phe	Met	Lys	Gln	Arg	Lys	Asn	Gln
			115					120					125			
25	Thr	Lys	Lys	Lys	Ala	Gln	Ile	Gln	Leu	Gln	His	Tyr	Val	Ser	Thr	
		130				135					140					
	Asp	Gly	Asp	Asp	Ile	Tyr	Val	Gly	Lys	Asn	Asn	Lys	Gln	Asn	Asp	Tyr
	145				150					155					160	
30	Leu	Thr	Asn	Lys	Lys	Ala	Lys	Lys	Thr	His	Thr	Trp	Leu	His	Thr	Lys
				165					170					175		
	Asp	Ile	Pro	Gly	Ser	His	Val	Val	Ile	Phe	Asn	Asp	Ala	Pro	Ser	Asp
				180					185					190		
35	Thr	Thr	Ile	Lys	Glu	Ala	Ala	Met	Leu	Ala	Gly	Tyr	Phe	Ser	Lys	Ala
			195					200					205			
40	Gly	Asn	Ser	Gly	Gln	Ile	Pro	Val	Asp	Tyr	Thr	Leu	Ile	Lys	Asn	Val
	210					215						220				
	His	Lys	Pro	Ser	Gly	Ala	Lys	Pro	Gly	Phe	Val	Thr	Tyr	Asp	Asn	Gln
	225				230					235					240	
45	Lys	Thr	Leu	Tyr	Ala											
				245												

(2) INFORMATION FOR SEQ ID NO:5223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5223:

Tyr Ile Thr Asn Pro Gln Asn Pro Lys Ile Lys Ile Thr Gly Ile Ser
 1 5 10 15
 Leu Ser Ser Gly Val Gly Asn Phe Phe Ile Ile Thr Asn Gly Lys Arg
 20 25 30
 Ile Ile Val Ala Lys Ile Lys Arg Asn Ala Asp Asn Asp Ser Ala Leu
 35 40 45
 Lys Ser Phe Asn Ala Ile Phe Ile Ile Gly Asn Ala Asp Pro His Asn
 50 55 60
 Met Ile Val Asn Lys Tyr Asp Arg Lys Val Val Ser Arg Ser Leu Phe
 65 70 75 80
 Ile Asn Ile Ile Thr Pro Leu Ile Met Cys Phe Tyr Ile Lys Lys Tyr
 85 90 95
 Asp Leu Lys

(2) INFORMATION FOR SEQ ID NO:5224:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5224:

Glu Asn Val Leu Ala Lys Glu Tyr Ala Val Lys Tyr Asn Ala Val Glu
 1 5 10 15
 Ala Ile Gln His Arg Gly Glu Thr Val Thr Glu Gly Ser Ser Ser Asn
 20 25 30
 Ala Tyr Ala Ile Lys Asp Gly Val Ile Tyr Thr His Pro Ile Asn Asn
 35 40 45
 Tyr Ile Leu Asn Gly Ile Thr Arg Ile Val Ile Lys Lys Ile Ala Glu
 50 55 60
 Asp Tyr Asn Ile Pro Phe Lys Glu Glu Thr Phe Thr Val Asp Phe Leu
 65 70 75 80
 Lys Asn Ala Asp Glu Val Ile Val Ser Ser Thr Ser Ala Glu Val Thr
 85 90 95
 Pro Val Ile Lys Leu Asp Gly Glu Pro Val Asn Asp Gly Lys Val Gly
 100 105 110

115

120

125

His Ser Ile
130

(2) INFORMATION FOR SEQ ID NO:5225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5225:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn
1 5 10 15
Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile
20 25 30
Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr
35 40 45
Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala
50 55 60
Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln
65 70 75 80
Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro
85 90 95
Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly
100 105 110
Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
115 120 125
Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
130 135 140
Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala
145 150 155 160
Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln
165 170 175
Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
180 185 190
Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
195 200 205

	210	215	220	
	Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly			
	225	230	235	240
5	Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn			
	245	250	255	
	Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val			
10	260	265	270	
	Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys			
	275	280	285	
15	Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr			
	290	295	300	
	Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp			
	305	310	315	320
20	Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly			
	325	330	335	
	Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu			
25	340	345	350	
	Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr			
	355	360	365	
	Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly			
30	370	375	380	
	Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro			
	385	390	395	400
35	Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn			
	405	410	415	
	Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu			
	420	425	430	
40	Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr			
	435	440	445	
	Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr			
45	450	455	460	
	Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly			
	465	470	475	480
	Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp			
50	485	490	495	
	Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr			
	500	505	510	
55	Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser			
	515	520	525	

530

535

540

(2) INFORMATION FOR SEQ ID NO:5226:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

- (ii) MOLECULE TYPE: protein

15

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5226:

Tyr Lys Glu Leu Ser His Gly Arg Leu Ile Gly Gly Thr Lys Met His
 1 5 10 15
 Lys Lys Tyr Phe Ile Gly Thr Ser Ile Leu Ile Ala Val Phe Val Val
 20 25 30
 Ile Phe Asp Gln Val Thr Lys Tyr Ile Ile Ala Thr Thr Met Lys Ile
 35 40 45
 Gly Asp Ser Phe Glu Val Ile Pro His Phe Leu Asn Ile Thr Ser His
 50 55 60
 Arg Asn Asn Gly Ala Ala Trp Gly Ile Leu Ser Gly Lys Met Thr Phe
 65 70 75 80
 Phe Phe Ile Ile Thr Ile Ile Ile Leu Ile Ala Leu Val Tyr Phe Phe
 85 90 95
 Ile Lys Asp Ala Gln Tyr Asn Leu Phe Met Gln Val Ala Ile Ser Leu
 100 105 110
 Leu Phe Ala Gly Ala Leu Gly Asn Phe Ile Asp Arg Ile Leu Thr Gly
 115 120 125
 Glu Val Val Asp Phe Ile Asp Thr Asn Ile Phe Gly Tyr Asp Phe Pro
 130 135 140
 Ile Phe Asn Ile Ala Asp Ser Ser Leu Thr Ile Gly Val Ile Leu Ile
 145 150 155 160
 Ile Ile Ala Leu Leu Lys Asp Thr Ser Asn Lys Lys Glu Lys Glu Val
 165 170 175
 Lys

50

(2) INFORMATION FOR SEQ ID NO:5227:

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5227:

Ala Gly Lys Ser Ser Leu Ile Lys Ser Leu Ile Gly Glu Phe Asn Ala
 1 5 10 15
 Thr Gly Thr Lys Leu Leu Tyr Asn Lys Pro Ile Gln Gln Gln Leu Gln
 20 25 30
 His Ile Thr Tyr Ile Pro Gln Lys Ala His Ile Asp Leu Asp Phe Pro
 35 40 45
 Ile Ser Val Glu Gln Val Ile Leu Ser Gly Cys Tyr Lys Glu Ile Gly
 50 55 60
 Trp Phe Arg Arg Pro Asn Lys Ser Ala Arg Asp Lys Leu Lys Gln Leu
 65 70 75 80
 Leu Ser Asp Leu Glu Leu Glu Ser Leu Arg His Arg Gln Ile Ser Glu
 85 90 95
 Leu Ser Gly Gly Gln Leu Gln Arg Val Leu Val Ala Arg Ala Leu Met
 100 105 110
 Ser Xaa Ser Glu Val Tyr Phe Leu Asp Glu Pro Phe Val Gly Ile Asp
 115 120 125
 Phe Ser Ser Glu Lys Leu Ile Met Thr Lys Ile Glu Asn Leu Lys Gln
 130 135 140
 Gln Gly Lys Leu Ile Leu Ile Ile His His Asp Leu Ser Lys Ala Lys
 145 150 155 160
 Gln Tyr Phe Asp Arg Ile Ile Leu Leu Asn Gln Thr Leu Arg Tyr Phe
 165 170 175
 Gly Asp Ser Glu Glu Ala Met Ser Val Thr Arg Leu Asn Glu Thr Phe
 180 185 190
 Met Ser Ser Thr Asp Cys Ser Asp Pro Ser Gln Arg Ser Asn Ile Thr
 195 200 205
 Cys

45

(2) INFORMATION FOR SEQ ID NO:5228:

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 256 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5228:

5 Thr Phe Arg Ile Ile Phe Leu Leu Ser Ile Arg Lys Arg Ser Asn Arg
 1 5 10 15
 Thr His Val Ser Ile His Trp Ser Thr Val Asn Lys Glu Glu Ile Cys
 20 25 30
 10 Leu Arg Val Lys Asp Asn Leu Gln Gln Ile Ser Thr Gln Ile Asn Asp
 35 40 45
 Lys Ser Glu Lys Asn Asn Phe Ser Thr Lys Pro Asn Val Ile Ala Val
 50 55 60
 15 Thr Lys Tyr Val Thr Ile Glu Arg Ala Lys Glu Ala Tyr Glu Ala Gly
 65 70 75 80
 Ile Arg His Phe Gly Glu Asn Arg Leu Glu Gly Phe Phe Gln Lys Lys
 85 90 95
 20 Glu Ala Leu Pro Ser Asp Ala Val Ile His Phe Ile Gly Ser Leu Gln
 100 105 110
 25 Ser Arg Lys Val Lys Asp Val Ile Asn Asp Val Asp Tyr Phe His Ala
 115 120 125
 Leu Asp Arg Leu Ser Leu Ala Lys Glu Ile Asn Lys Arg Ala Glu His
 130 135 140
 30 Lys Ile Lys Cys Phe Leu Gln Val Asn Val Ser Gly Glu Ala Ser Lys
 145 150 155 160
 His Gly Ile Ala Leu Glu Asp Val Asp Gln Phe Ile Asp Asp Leu Lys
 165 170 175
 35 Lys Tyr Asp Lys Ile Glu Ile Val Gly Leu Met Thr Met Ala Pro Leu
 180 185 190
 Thr Asp Asp Glu Ala Tyr Ile Arg Ser Leu Phe Lys Gln Leu Arg Leu
 195 200 205
 40 Lys Lys Glu Glu Ile Gln Arg Leu Asn Leu Glu Tyr Ala Pro Cys Asp
 210 215 220
 45 Glu Leu Ser Met Gly Met Ser Asn Asp Tyr Leu Ile Ala Val Glu Glu
 225 230 235 240
 Gly Ala Thr Phe Val Arg Ile Gly Thr Lys Leu Val Gly Glu Glu Glu
 245 250 255

(2) INFORMATION FOR SEQ ID NO:5229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5229:

10 Lys His Lys Leu Thr Ile Ile Thr Gly Gly Phe Phe Thr Met Lys Lys
 1 5 10 15
 Thr Ile Met Ala Ser Ser Leu Ala Val Ala Leu Gly Val Thr Gly Tyr
 20 25 30
 15 Ala Ala Gly Thr Gly His Gln Ala His Ala Ala Glu Val Asn Val Asp
 35 40 45
 Gln Ala His Leu Val Asp Leu Ala His Asn His Gln Asp Gln Leu Asn
 50 55 60
 20 Ala Ala Pro Ile Lys Asp Gly Ala Tyr Asp Ile His Phe Val Lys Asp
 65 70 75 80
 Gly Phe Gln Tyr Asn Phe Thr Ser Asn Gly Thr Thr Trp Ser Trp Ser
 85 90 95
 25 Tyr Glu Ala Ala Asn Gly Gln Thr Ala Gly Phe Ser Asn Val Ala Gly
 100 105 110
 Ala Asp Tyr Thr Thr Ser Tyr Asn Gln Gly Ser Asn Val Gln Ser Val
 115 120 125
 Ser Tyr Asn Ala Gln Ser Ser Asn Ser Asn Val Glu Ala Val Ser Ala
 130 135 140
 35 Pro Thr Tyr His Asn Tyr Ser Thr Ser Thr Thr Ser Ser Ser Val Arg
 145 150 155 160
 Leu Ser Asn Gly Asn Thr Ala Gly Ala Thr Gly Ser Ser Ala Ala Gln
 165 170 175
 40 Ile Met Ala Gln Arg Thr Gly Val Ser Ala Ser Thr Trp Ala Ala Ile
 180 185 190
 Ile Ala Arg Glu Ser Asn Gly Gln Val Asn Ala Tyr Asn Pro Ser Gly
 195 200 205
 45 Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly Pro Thr Asn Thr
 210 215 220
 Val Asp Gln Gln Ile Asn Ala Ala Val Lys Ala Tyr Lys Ala Gln Gly
 225 230 235 240
 50 Leu Gly Ala Trp Gly Phe
 245

(2) INFORMATION FOR SEQ ID NO:5230:

55

(A) LENGTH: 519 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5230:

```

Lys Glu Pro His Lys Met Lys Lys Ile Tyr Lys Ser Leu Thr Val Ser
 1           5           10           15
Ala Ile Val Ala Thr Val Ser Leu Ser Ala Leu Pro Gln Ser Leu Ala
15          20          25          30
Ile Thr His Glu Ser Gln Pro Thr Lys Gln Gln Arg Thr Val Leu Phe
20          35          40          45
Asp Arg Ser His Gly Gln Thr Ala Gly Ala Ala Asp Trp Val Ser Asp
25          50          55          60
Gly Ala Phe Ser Asp Tyr Ala Asp Ser Ile Gln Lys Gln Gly Tyr Asp
25          65          70          75          80
Val Lys Ala Ile Asp Gly His Ser Asn Ile Thr Glu Ala Ser Leu Lys
          85          90          95
Ser Ser Lys Ile Phe Val Ile Pro Glu Ala Asn Ile Pro Phe Lys Glu
30          100         105         110
Ser Glu Gln Ala Ala Ile Val Lys Tyr Val Lys Gln Gly Gly Asn Val
          115         120         125
Val Phe Ile Ser Asp His Tyr Asn Ala Asp Arg Asn Leu Asn Arg Ile
35          130         135         140
Asp Ser Ser Glu Ala Met Asn Gly Tyr Arg Arg Gly Ala Tyr Glu Asp
          145         150         155         160
Met Ser Lys Gly Met Asn Ala Glu Glu Lys Ser Ser Thr Ala Met Gln
40          165         170         175
Gly Val Lys Ser Ser Asp Trp Leu Ser Thr Asn Phe Gly Val Arg Phe
45          180         185         190
Arg Tyr Asn Ala Leu Gly Asp Leu Asn Thr Ser Asn Ile Val Ser Ser
          195         200         205
Lys Glu Ser Phe Gly Ile Thr Glu Gly Val Lys Ser Val Ser Met His
50          210         215         220         225         240
Ala Gly Ser Thr Leu Ala Ile Thr Asn Pro Glu Lys Ala Lys Gly Ile
          225         230         235
Val Tyr Thr Pro Glu Gln Leu Pro Ala Lys Ser Lys Trp Ser His Ala
55          245         250         255

```

Val Asp Gln Gly Ile Tyr Asn Gly Gly Gly Lys Ala Glu Gly Pro Tyr
 260 265 270
 Val Ala Ile Ser Lys Val Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp
 275 280 285
 Ser Ser Leu Val Glu Asp Ser Ser Pro Lys Tyr Val Arg Glu Asp Asn
 290 295 300
 Gly Glu Lys Lys Lys Thr Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly
 305 310 315 320
 Lys Leu Leu Asn Asn Ile Thr Ala Trp Met Ser Lys Asp Asn Asp Gly
 325 330 335
 Lys Ser Leu Lys Ala Ser Ser Leu Thr Leu Asp Thr Lys Thr Lys Leu
 340 345 350
 Leu Asp Phe Glu Arg Pro Glu Arg Ser Thr Glu Pro Glu Lys Glu Pro
 355 360 365
 Trp Ser Gln Pro Pro Ser Gly Tyr Lys Trp Tyr Asp Pro Thr Thr Phe
 370 375 380
 Lys Ala Gly Ser Tyr Gly Ser Glu Lys Gly Ala Asp Pro Gln Pro Asn
 385 390 395 400
 Thr Pro Asp Asp His Thr Pro Pro Asn Gln Asn Glu Lys Val Thr Phe
 405 410 415
 Asp Ile Pro Gln Asn Val Ser Val Asn Glu Pro Phe Glu Met Thr Ile
 420 425 430
 His Leu Lys Gly Phe Glu Ala Asn Gln Thr Leu Glu Asn Leu Arg Val
 435 440 445
 Gly Ile Tyr Lys Glu Gly Gly Arg Gln Ile Gly Gln Phe Ser Ser Lys
 450 455 460
 Asp Asn Asp Tyr Asn Pro Pro Gly Tyr Ser Thr Leu Pro Thr Val Lys
 465 470 475 480
 Ala Asp Glu Asn Gly Asn Val Thr Ile Lys Val Asn Ala Lys Val Leu
 485 490 495
 Glu Ser Met Glu Gly Ser Lys Ile Arg Leu Lys Leu Gly Asp Lys Thr
 500 505 510
 Leu Ile Thr Thr Asp Phe Lys
 515

(2) INFORMATION FOR SEQ ID NO:5231:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5231:

5 Arg Asp Glu Arg Ile Lys Thr Met Thr Asn Ser Ser Lys Ser Phe Thr
 1 5 10 15
 Lys Phe Met Ala Ala Ser Ala Val Phe Thr Met Gly Phe Leu Ser Val
 20 25 30
 10 Pro Thr Ala Gly Ala Glu Gln Thr Asn Gln Ile Ala Asn Lys Pro Gln
 35 40 45
 Ala Ile Gln Trp His Thr Asn Leu Thr Asn Glu Arg Phe Thr Thr Ile
 50 55 60
 15 Ala His Arg Gly Ala Ser Gly Tyr Ala Pro Glu His Thr Phe Gln Ala
 65 70 75 80
 Tyr Asp Lys Ser His Asn Glu Leu Lys Ala Ser Tyr Ile Glu Ile Asp
 85 90 95
 20 Leu Gln Arg Thr Lys Asp Gly His Leu Val Ala Met His Asp Glu Thr
 100 105 110
 25 Val Asn Arg Thr Thr Asn Gly His Gly Lys Val Glu Asp Tyr Thr Leu
 115 120 125
 Asp Glu Leu Lys Gln Leu Asp Ala Gly Ser Trp Phe Asn Lys Lys Tyr
 130 135 140
 30 Pro Lys Tyr Ala Arg Ala Ser Tyr Lys Asn Ala Lys Val Pro Thr Leu
 145 150 155 160
 Asp Glu Ile Leu Glu Arg Tyr Gly Pro Asn Ala Asn Tyr Tyr Ile Glu
 165 170 175
 35 Thr Lys Ser Pro Asp Val Tyr Pro Gly Met Glu Glu Gln Leu Leu Ala
 180 185 190
 40 Ser Leu Lys Lys His His Leu Leu Asn Asn Asn Lys Leu Lys Asn Gly
 195 200 205
 His Val Met Ile Gln Ser Phe Ser Asp Glu Ser Leu Lys Lys Ile His
 210 215 220
 45 Arg Gln Asn Lys His Val Pro Leu Val Lys Leu Val Asp Lys Gly Glu
 225 230 235
 Leu Gln Gln Phe Asn Asp Gln Arg Leu Lys Glu Ile Arg Ser Tyr Ala
 245 250 255
 50 Ile Gly Leu Gly Pro Asp Tyr Thr Asp Leu Thr Glu Gln Asn Thr His
 260 265 270
 55 His Leu Lys Asp Leu Gly Phe Ile Val His Pro Tyr Thr Val Asn Glu
 275 280 285

Lys Ala Asp Met Leu Arg Leu Asn Lys Tyr Gly Val Asp Gly Val Phe
 290 295 300

Thr Asn Phe Ala Asp Lys Tyr Lys Glu Val Ile Lys
 305 310 315

(2) INFORMATION FOR SEQ ID NO:5232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5232:

Arg Phe Met Lys Asn Leu Ile Ser Ile Ile Ile Ile Leu Cys Leu Thr
 1 5 10 15
 Leu Ser Ile Met Thr Pro Tyr Ala Gln Ala Thr Asn Ser Asp Val Thr
 20 25 30
 Pro Val Gln Ala Ala Asn Gln Tyr Gly Tyr Ala Gly Leu Ser Ala Ala
 35 40 45
 Tyr Glu Pro Thr Ser Ala Val Asn Val Ser Gln Thr Gly Gln Leu Leu
 50 55 60
 Tyr Gln Tyr Asn Ile Asp Thr Lys Trp Asn Pro Ala Ser Met Thr Lys
 65 70 75 80
 Leu Met Thr Met Tyr Leu Thr Leu Glu Ala Val Asn Lys Gly Gln Leu
 85 90 95
 Ser Leu Asp Asp Thr Val Thr Met Thr Asn Lys Glu Tyr Ile Met Ser
 100 105 110
 Thr Leu Pro Glu Leu Ser Asn Thr Lys Leu Tyr Pro Gly Gln Val Trp
 115 120 125
 Thr Ile Ala Asp Leu Leu Gln Ile Thr Val Ser Asn Ser Ser Asn Ala
 130 135 140
 Ala Ala Leu Ile Leu Ala Lys Lys Val Ser Lys Asn Thr Ser Asp Phe
 145 150 155 160
 Val Asp Leu Met Asn Asn Lys Ala Lys Ala Ile Gly Met Lys Asn Thr
 165 170 175
 His Phe Val Asn Pro Thr Gly Ala Glu Asn Ser Arg Leu Arg Thr Phe
 180 185 190
 Ala Pro Thr Lys Tyr Lys Asp Gln Glu Arg Thr Val Thr Thr Ala Arg
 195 200 205

```

      Asp Tyr Ala Ile Leu Asp Leu His Val Ile Lys Glu Thr Pro Lys Ile
      210                215                220
5      Leu Asp Phe Thr Lys Gln Leu Ala Pro Thr Thr His Ala Val Thr Tyr
      225                230                235                240
      Tyr Thr Phe Asn Phe Ser Leu Glu Gly Ala Lys Met Ser Leu Pro Gly
      245                250                255
10     Thr Asp Gly Leu Lys Thr Gly Ser Ser Asp Thr Ala Asn Tyr Asn His
      260                265                270
      Thr Ile Thr Thr Lys Arg Gly Lys Phe Arg Ile Asn Gln Val Ile Met
      275                280                285
15     Gly Ala Gly Asp Tyr Lys Asn Leu Gly Gly Glu Lys Gln Arg Asn Met
      290                295                300
      Met Gly Asn Ala Leu Met Glu Arg Ser Phe Asp Gln Tyr Lys Tyr Val
      305                310                315                320
20     Lys Ile Leu Ser Lys Gly Glu Gln Arg Ile Asn Gly Lys Lys Tyr Tyr
      325                330                335
      Val Glu Asn Asp Leu Tyr Asp Val Leu Pro Ser Asp Phe Ser Lys Lys
      340                345                350
25     Asp Tyr Lys Leu Val Val Glu Asp Gly Lys Val His Ala Asp Tyr Pro
      355                360                365
      Arg Glu Phe Ile Asn Lys Asp Tyr Gly Pro Pro Thr Val Glu Val His
      370                375                380
30     Gln Pro Ile Ile Gln Lys Ala Asn Thr Val Ala Lys Ser Met Trp Glu
      385                390                395                400
35     Glu His Pro Leu Phe Thr Ile Ile Gly Gly Thr Cys Leu Val Ala Gly
      405                410                415
      Leu Ala Leu Ile Val His Met Ile Ile Asn Arg Leu Phe Arg Lys Arg
      420                425                430
40     Lys

```

(2) INFORMATION FOR SEQ ID NO:5233:

- ```

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5233:

```

Leu Thr Lys Glu Arg Glu Tyr Met Lys Leu Lys Ser Phe Ile Thr Val  
 1 5 10 15  
 5 Thr Leu Ala Leu Gly Met Ile Ala Thr Thr Gly Ala Thr Val Ala Gly  
 20 25 30  
 Asn Glu Val Ser Ala Ala Glu Lys Asp Lys Leu Pro Ala Thr Gln Lys  
 35 40 45  
 10 Ala Lys Glu Met Gln Asn Val Pro Tyr Thr Ile Ala Val Asp Gly Ile  
 50 55 60  
 Met Ala Phe Asn Gln Ser Tyr Leu Asn Leu Pro Lys Asp Ser Gln Leu  
 65 70 75 80  
 15 Ser Tyr Leu Asp Leu Gly Asn Lys Val Lys Ala Leu Leu Tyr Asp Glu  
 85 90 95  
 Arg Gly Val Thr Pro Glu Lys Ile Arg Asn Ala Lys Ser Ala Val Tyr  
 100 105 110  
 20 Thr Ile Thr Trp Lys Asp Gly Ser Lys Lys Glu Val Asp Leu Lys Lys  
 115 120 125  
 Asp Ser Tyr Thr Ala Asn Leu Phe Asp Ser Asn Ser Ile Lys Gln Ile  
 130 135 140  
 25 Asp Ile Asn Val Lys Thr Lys  
 145 150

## (2) INFORMATION FOR SEQ ID NO:5234:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 497 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5234:

Asn His Cys Asn Arg Ile Glu Arg Lys Met Ala Met Ser Asn Asn Phe  
 1 5 10 15  
 45 Lys Asp Asp Phe Glu Lys Asn Arg Gln Ser Ile Asp Thr Asn Ser His  
 20 25 30  
 Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln Ser Glu Leu Glu His  
 35 40 45  
 50 Gln Asp Thr Ile Glu Asn Thr Glu Gln Gln Phe Pro Pro Arg Asn Ala  
 50 55 60  
 55 Gln Arg Arg Lys Arg Arg Arg Asp Leu Ala Thr Asn His Asn Lys Gln  
 65 70 75 80

Val His Asn Glu Ser Gln Thr Ser Glu Asp Asn Val Gln Asn Glu Ala  
85 90 95

5 Gly Thr Ile Asp Asp Arg Gln Val Glu Ser Ser His Ser Thr Glu Ser  
100 105 110

Gln Glu Pro Ser His Gln Asp Ser Thr Pro Gln His Glu Glu Glu Tyr  
115 120 125

10 Tyr Asn Lys Asn Ala Phe Ala Met Asp Lys Ser His Pro Glu Pro Ile  
130 135 140

Glu Asp Asn Asp Lys His Asp Thr Ile Lys Asn Ala Glu Asn Asn Thr  
145 150 155 160

15 Glu His Ser Thr Val Ser Asp Lys Ser Glu Ala Glu Gln Ser Gln Gln  
165 170 175

Pro Lys Pro Tyr Phe Thr Thr Gly Ala Asn Gln Ser Glu Thr Ser Lys  
180 185 190

20 Asn Glu His Asp Asn Asp Ser Val Lys Gln Asp Gln Asp Glu Pro Lys  
195 200 205

Glu His His Asn Gly Lys Lys Ala Ala Ala Ile Gly Ala Gly Thr Ala  
210 215 220 240

Gly Val Ala Gly Ala Ala Gly Ala Met Ala Ala Ser Lys Ala Lys Lys  
225 230 235 240

30 His Ser Asn Asp Ala Gln Asn Lys Ser Asn Ser Gly Lys Ala Asn Asn  
245 250 255

Ser Thr Glu Asp Lys Ala Ser Gln Asp Lys Ser Lys Asp His His Asn  
260 265 270

35 Gly Lys Lys Gly Ala Ala Ile Gly Ala Gly Thr Ala Gly Leu Ala Gly  
275 280 285

Gly Ala Ala Ser Lys Ser Ala Ser Ala Ala Ser Lys Pro His Ala Ser  
290 295 300

40 Asn Asn Ala Ser Gln Asn His Asp Glu His Asp Asn His Asp Arg Asp  
305 310 315 320

Lys Glu Arg Lys Lys Gly Gly Met Ala Lys Val Leu Leu Pro Leu Ile  
325 330 335

45 Ala Ala Val Leu Ile Ile Gly Ala Leu Ala Ile Phe Gly Gly Met Ala  
340 345 350

Leu Asn Asn His Asn Asn Gly Thr Lys Glu Asn Lys Ile Ala Asn Thr  
355 360 365

50 Asn Lys Asn Asn Ala Asp Glu Ser Lys Asp Lys Asp Thr Ser Lys Asp  
370 375 380

55 Ala Ser Lys Asp Lys Ser Lys Ser Thr Asp Ser Asp Lys Ser Lys Glu  
385 390 395 400



Asp Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp Asn Asp Gln Asn Asn  
 405 410 415  
 Ala Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn Gln Asn Gln Gln  
 420 425 430  
 Ala Asn Gln Asn Gln Gln Gln Gln Gln Arg Gln Gly Gly Gln  
 435 440 445  
 Arg His Thr Val Asn Gly Gln Glu Asn Leu Tyr Arg Ile Ala Ile Gln  
 450 455 460  
 Tyr Tyr Gly Ser Gly Ser Pro Glu Asn Val Glu Lys Ile Arg Arg Ala  
 465 470 475 480  
 Asn Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly Gln Gln Ile Val Ile  
 485 490 495  
 Pro

20

## (2) INFORMATION FOR SEQ ID NO:5235:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 886 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5235:

Leu Leu Ser Ile Lys Tyr Asn Leu Ile Gly Val Val Asn Asn Met Asn  
 1 5 10 15  
 Lys His His Pro Lys Leu Arg Ser Phe Tyr Ser Ile Arg Lys Ser Thr  
 20 25 30  
 Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile Thr Ser  
 35 40 45  
 Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Thr Ser Asp Lys Ile  
 50 55 60  
 Ser Glu Asn Gln Asn Asn Asn Ala Thr Thr Thr Gln Pro Pro Lys Asp  
 65 70 75 80  
 Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Ala Asn Thr Ala Lys Asn  
 85 90 95  
 Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp Pro Ala  
 100 105 110  
 Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val Asn Phe  
 115 120 125

55

Gln Leu Leu Asp Lys Asn Asn Glu Thr Gln Tyr Tyr His Phe Phe Ser  
 130 135 140  
 Ile Lys Asp Pro Ala Asp Val Tyr Tyr Thr Lys Lys Lys Ala Glu Val  
 145 150 155 160  
 Glu Leu Asp Ile Asn Thr Ala Ser Thr Trp Lys Lys Phe Glu Val Tyr  
 165 170 175  
 Glu Asn Asn Gln Lys Leu Pro Val Arg Leu Val Ser Tyr Ser Pro Val  
 180 185 190  
 Pro Glu Asp His Ala Tyr Ile Arg Phe Pro Val Ser Asp Gly Thr Gln  
 195 200 205  
 Glu Leu Lys Ile Val Ser Ser Thr Gln Ile Asp Asp Gly Glu Glu Thr  
 210 215 220  
 Asn Tyr Asp Tyr Thr Lys Leu Val Phe Ala Lys Pro Ile Tyr Asn Asp  
 225 230 235 240  
 Pro Ser Leu Val Lys Ser Asp Thr Asn Asp Ala Val Val Thr Asn Asp  
 245 250 255  
 Gln Ser Ser Ser Val Ala Ser Asn Gln Thr Asn Thr Asn Thr Ser Asn  
 260 265 270  
 Gln Asn Ile Ser Thr Ile Asn Asn Ala Asn Asn Gln Pro Gln Ala Thr  
 275 280 285  
 Thr Asn Met Ser Gln Pro Ala Gln Pro Lys Ser Ser Thr Asn Ala Asp  
 290 295 300  
 Gln Ala Ser Ser Gln Pro Ala His Glu Thr Asn Ser Asn Gly Asn Thr  
 305 310 315 320  
 Asn Asp Lys Thr Asn Glu Ser Ser Asn Gln Ser Asp Val Asn Gln Gln  
 325 330 335  
 Tyr Pro Pro Ala Asp Glu Ser Leu Gln Asp Ala Ile Lys Asn Pro Ala  
 340 345 350  
 Ile Ile Asp Lys Glu His Thr Ala Asp Asn Trp Arg Pro Ile Asp Phe  
 355 360 365  
 Gln Met Lys Asn Asp Lys Gly Glu Arg Gln Phe Tyr His Tyr Ala Ser  
 370 375 380  
 Thr Val Glu Pro Ala Thr Val Ile Phe Thr Lys Thr Gly Pro Ile Ile  
 385 390 395 400  
 Glu Leu Gly Leu Lys Thr Ala Ser Thr Trp Lys Lys Phe Glu Val Tyr  
 405 410 415  
 Glu Gly Asp Lys Lys Leu Pro Val Glu Leu Val Ser Tyr Asp Ser Asp  
 420 425 430  
 Lys Asp Tyr Ala Tyr Ile Arg Phe Pro Val Ser Asn Gly Thr Arg Glu  
 435 440 445

Val Lys Ile Val Ser Ser Ile Glu Tyr Gly Glu Asn Ile His Glu Asp  
 450 455 460

5 Tyr Asp Tyr Thr Leu Met Val Phe Ala Gln Pro Ile Thr Asn Asn Pro  
 465 470 475 480

Asp Asp Tyr Val Asp Glu Glu Thr Tyr Asn Leu Gln Lys Leu Leu Ala  
 485 490 495

10 Pro Tyr His Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Glu  
 500 505 510

Lys Leu Gln Glu Lys Leu Pro Glu Lys Tyr Lys Ala Glu Tyr Lys Lys  
 515 520 525

15 Lys Leu Asp Gln Thr Arg Val Glu Leu Ala Asp Gln Val Lys Ser Ala  
 530 535 540

Val Thr Glu Phe Glu Asn Val Thr Pro Thr Asn Asp Gln Leu Thr Asp  
 545 550 555 560

20 Leu Gln Glu Ala His Phe Val Val Phe Glu Ser Glu Glu Asn Ser Glu  
 565 570 575

Ser Val Met Asp Gly Phe Val Glu His Pro Phe Tyr Thr Ala Thr Leu  
 580 585 590

25 Asn Gly Gln Lys Tyr Val Val Met Lys Thr Lys Asp Asp Ser Tyr Trp  
 595 600 605

30 Lys Asp Leu Ile Val Glu Gly Lys Arg Val Thr Thr Val Ser Lys Asp  
 610 615 620

Pro Lys Asn Asn Ser Arg Thr Leu Ile Phe Pro Tyr Ile Pro Asp Lys  
 625 630 635 640

35 Ala Val Tyr Asn Ala Ile Val Lys Val Val Ala Asn Ile Gly Tyr  
 645 650 655

Glu Gly Gln Tyr His Val Arg Ile Ile Asn Gln Asp Ile Asn Thr Lys  
 660 665 670

40 Asp Asp Asp Thr Ser Gln Asn Asn Thr Ser Glu Pro Leu Asn Val Gln  
 675 680 685

Thr Gly Gln Glu Gly Lys Val Ala Asp Thr Asp Val Ala Glu Asn Ser  
 690 695 700

45 Ser Thr Ala Thr Asn Pro Lys Asp Ala Ser Asp Lys Ala Asp Val Ile  
 705 710 715 720

Glu Pro Glu Ser Asp Val Val Lys Asp Ala Asp Asn Asn Ile Asp Lys  
 725 730 735

50 Asp Val Gln His Asp Val Asp His Leu Ser Asp Met Ser Asp Asn Asn  
 740 745 750

55 His Phe Asp Lys Tyr Asp Leu Lys Glu Met Asp Thr Gln Ile Ala Lys  
 755 760 765

Asp Thr Asp Arg Asn Val Asp Lys Asp Ala Asp Asn Ser Val Gly Met  
 770 775 780  
 Ser Ser Asn Val Asp Thr Asp Lys Asp Ser Asn Lys Asn Lys Asp Lys  
 785 790 795 800  
 Val Ile Gln Leu Asn His Ile Ala Asp Lys Asn Asn His Thr Gly Lys  
 805 810 815  
 Ala Ala Lys Leu Asp Val Val Lys Gln Asn Tyr Asn Asn Thr Asp Lys  
 820 825 830  
 Val Thr Asp Lys Lys Thr Thr Glu His Leu Pro Ser Asp Ile His Lys  
 835 840 845  
 Thr Val Asp Lys Thr Val Lys Thr Lys Glu Lys Ala Gly Thr Pro Ser  
 850 855 860  
 Lys Glu Asn Lys Leu Ser Gln Ser Lys Met Leu Thr Lys Asn Trp Arg  
 865 870 875 880  
 Asn Asn Xaa Gln Ala Asn  
 885

## (2) INFORMATION FOR SEQ ID NO:5236:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 236 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5236:  
 Asn Met Asn Lys Asn Val Met Val Lys Gly Leu Thr Ala Leu Thr Ile  
 1 5 10 15  
 Leu Thr Ser Leu Gly Phe Ala Glu Asn Ile Ser Asn Gln Xaa His Ser  
 20 25 30  
 Ile Ala Lys Ala Glu Lys Asn Val Lys Glu Ile Thr Asp Ala Thr Lys  
 35 40 45  
 Glu Pro Tyr Asn Ser Val Val Ala Phe Val Gly Gly Thr Gly Val Val  
 50 55 60  
 Val Gly Lys Asn Thr Ile Val Thr Asn Lys His Ile Ala Lys Ser Asn  
 65 70 75 80  
 Asp Ile Phe Lys Asn Arg Val Ser Ala His His Ser Ser Lys Gly Lys  
 85 90 95  
 Gly Gly Gly Asn Tyr Asp Val Lys Asp Ile Val Glu Tyr Pro Gly Lys  
 100 105 110

Glu Asp Leu Ala Ile Val His Val His Glu Thr Ser Thr Glu Gly Leu  
 115 120 125  
 Asn Phe Asn Lys Asn Val Ser Tyr Thr Lys Phe Ala Asp Gly Ala Lys  
 130 135 140  
 Val Lys Asp Arg Ile Ser Val Ile Gly Tyr Pro Lys Gly Ala Gln Thr  
 145 150 155 160  
 Lys Tyr Lys Met Phe Glu Ser Thr Gly Thr Ile Asn His Ile Ser Gly  
 165 170 175  
 Thr Phe Met Glu Phe Asp Ala Tyr Ala Gln Pro Gly Asn Ser Gly Ser  
 180 185 190  
 Pro Val Leu Asn Ser Lys His Xaa Leu Ile Gly Ile Leu Tyr Ala Gly  
 195 200 205  
 Ser Gly Lys Asp Glu Ser Glu Lys Asn Phe Gly Val Tyr Phe Thr Pro  
 210 215 220  
 Gln Leu Xaa Xaa Phe Ile Pro Asn Asn Ile Glu Lys  
 225 230 235

## (2) INFORMATION FOR SEQ ID NO:5237:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 363 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5237:

Tyr Arg Leu Glu His Thr Ile Met Lys Met Arg Thr Ile Ala Lys Thr  
 1 5 10 15  
 Ser Leu Ala Leu Gly Leu Leu Thr Thr Gly Ala Ile Thr Val Thr Thr  
 20 25 30  
 Gln Ser Val Lys Ala Glu Lys Ile Gln Ser Thr Lys Val Asp Lys Val  
 35 40 45  
 Pro Thr Leu Lys Ala Glu Arg Leu Ala Met Ile Asn Ile Thr Ala Gly  
 50 55 60  
 Ala Asn Ser Ala Thr Thr Gln Ala Ala Asn Thr Arg Gln Glu Arg Thr  
 65 70 75 80  
 Pro Lys Leu Glu Lys Ala Pro Asn Thr Asn Glu Glu Lys Thr Ser Ala  
 85 90 95  
 Ser Lys Ile Glu Lys Ile Ser Gln Pro Lys Gln Glu Glu Gln Lys Thr  
 100 105 110

Leu Asn Ile Ser Ala Thr Pro Ala Pro Lys Gln Glu Gln Ser Gln Thr  
 115 120 125  
 5 Thr Thr Glu Ser Thr Thr Pro Lys Thr Lys Val Thr Thr Pro Pro Ser  
 130 135 140  
 Thr Asn Thr Pro Gln Pro Met Gln Ser Thr Lys Ser Asp Thr Pro Gln  
 145 150 155 160  
 10 Ser Pro Thr Ile Lys Gln Ala Gln Thr Asp Met Thr Pro Lys Thr Glu  
 165 170 175  
 Asp Leu Arg Ala Tyr Tyr Thr Lys Pro Ser Phe Glu Phe Glu Lys Gln  
 180 185 190  
 15 Phe Gly Phe Met Leu Lys Pro Trp Thr Thr Val Arg Phe Met Asn Val  
 195 200 205  
 Ile Pro Asn Arg Phe Ile Tyr Lys Ile Ala Leu Val Gly Lys Asp Glu  
 210 215 220  
 20 Lys Lys Tyr Lys Asp Gly Pro Tyr Asp Asn Ile Asp Val Phe Ile Val  
 225 230 235 240  
 25 Leu Glu Asp Asn Lys Tyr Gln Leu Lys Lys Tyr Ser Val Gly Gly Ile  
 245 250 255  
 Thr Lys Thr Asn Ser Lys Lys Val Asn His Lys Val Glu Leu Ser Ile  
 260 265 270  
 30 Thr Lys Lys Asp Asn Gln Gly Met Ile Ser Arg Asp Val Ser Glu Tyr  
 275 280 285  
 Met Ile Thr Lys Glu Glu Ile Ser Leu Lys Glu Leu Asp Phe Lys Leu  
 290 295 300  
 35 Arg Lys Gln Leu Ile Glu Lys His Asn Leu Tyr Gly Asn Met Gly Ser  
 305 310 315 320  
 40 Gly Thr Ile Val Ile Lys Met Lys Asn Gly Gly Lys Tyr Thr Phe Glu  
 325 330 335  
 Leu His Lys Lys Leu Gln Glu His Arg Met Ala Asp Val Ile Asp Gly  
 340 345 350  
 45 Thr Asn Ile Asp Asn Ile Glu Val Asn Ile Lys  
 355 360

## (2) INFORMATION FOR SEQ ID NO:5238:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5238:

5 Phe Met Lys Phe Lys Ser Leu Ile Thr Thr Leu Ala Leu Gly Val  
 1 5 10 15  
 Leu Ala Ser Thr Gly Ala Asn Phe Asn Asn Asn Glu Ala Ser Ala Ala  
 20 25 30  
 10 Ala Lys Pro Leu Asp Lys Ser Ser Ser Ser Leu His His Gly Tyr Ser  
 35 40 45  
 Lys Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn  
 50 55 60  
 15 Ile Leu Ser Ser Leu Thr Phe Asn Lys Asn Gln Asn Ile Ser Tyr Lys  
 65 70 75 80  
 Asp Leu Glu Asp Arg Val Lys Ser Val Leu Lys Ser Asp Arg Gly Ile  
 85 90 95  
 20 Ser Asp Ile Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Tyr  
 100 105 110  
 Phe Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr  
 115 120 125  
 25 Thr Ala Asp Leu Ile Asn Thr Ser Glu Ile Lys Ala Ile Asn Ile Asn  
 130 135 140  
 Val Asp Thr Lys Lys Gln  
 145 150  
 30

## (2) INFORMATION FOR SEQ ID NO:5239:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 239 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5239:

45 Glu Lys Arg Phe Met Gln Met Ala Arg Lys Val Val Val Val Asp Asp  
 1 5 10 15  
 Glu Lys Pro Ile Ala Asp Ile Leu Glu Phe Asn Leu Lys Lys Gly  
 20 25 30  
 50 Tyr Asp Val Tyr Cys Ala Tyr Asp Gly Asn Asp Ala Val Asp Leu Ile  
 35 40 45  
 Tyr Glu Glu Glu Pro Asp Ile Val Leu Leu Asp Ile Met Leu Pro Gly  
 50 55 60  
 55

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 Arg Asp Gly Met Glu Val Cys Arg Glu Val Arg Lys Lys Tyr Glu Met
 65 70 75 80
5 Pro Ile Ile Met Leu Thr Ala Lys Asp Ser Glu Ile Asp Lys Val Leu
 85 90
 Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys Pro Phe Ser Thr
 100 105 110
10 Arg Glu Leu Ile Ala Arg Val Lys Ala Asn Leu Arg Arg His Tyr Ser
 115 120 125
 Gln Pro Ala Gln Asp Thr Gly Asn Val Thr Asn Glu Ile Thr Ile Lys
 130 135 140
15 Asp Ile Val Ile Tyr Pro Asp Ala Tyr Ser Ile Lys Lys Arg Gly Glu
 145 150 155 160
 Asp Ile Glu Leu Thr His Arg Glu Phe Glu Leu Phe His Tyr Leu Ser
 165 170 175
20 Lys His Met Gly Gln Val Met Thr Arg Glu His Leu Leu Gln Thr Val
 180 185 190
 Trp Gly Tyr Asp Tyr Phe Gly Asp Val Arg Thr Val Asp Val Thr Ile
 195 200 205
25 Arg Arg Leu Arg Glu Lys Ile Glu Asp Asp Pro Ser His Pro Glu Tyr
 210 215 220
 Ile Val Thr Arg Arg Gly Val Gly Tyr Phe Leu Gln Gln His Glu
 225 230 235
30

```

## (2) INFORMATION FOR SEQ ID NO:5240:

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 (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 133 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
40
 (ii) MOLECULE TYPE: protein
45
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5240:
 Xaa Leu Ser Thr Val Ile Gly Ala Xaa Leu Phe Phe Lys Ser Ser Val
 1 5 10
50 Ser Leu Val Phe Lys Met Val Lys Lys Phe Arg Xaa Gly Val Ile Ser
 20 25 30
 Val Asn Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys
 35 40 45
55 Asn Ala Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val
 50 55 60

```



Ser Val Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu  
 65 70 75 80  
 Ile Lys Tyr Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys  
 85 90 95  
 Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe  
 100 105 110  
 Tyr Asn Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu  
 115 120 125  
 Phe Asp Val Lys Ala  
 130

15

(2) INFORMATION FOR SEQ ID NO:5241:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 508 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein

25

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:5241:

Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val  
 1 5 10 15  
 Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe Ile Asn Gly  
 20 25 30  
 Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro  
 35 40 45  
 Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp  
 50 55 60  
 Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser  
 65 70 75 80  
 Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp  
 85 90 95  
 Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn  
 100 105 110  
 Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala  
 115 120 125  
 Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly  
 130 135 140  
 Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu  
 145 150 155 160

55

Pro Ile Gly Val Val Gly Ala Val Val Ala Trp Asn Phe Pro Met Leu  
 165 170 175  
 5 Leu Ala Ala Trp Lys Ile Ala Pro Ala Ile Ala Ala Gly Asn Thr Ile  
 180 185 190  
 Val Ile Gln Pro Ser Ser Ser Thr Pro Leu Ser Leu Leu Glu Val Ala  
 195 200 205  
 10 Lys Ile Phe Gln Glu Val Leu Pro Lys Gly Val Val Asn Ile Leu Thr  
 210 215 220  
 Gly Lys Gly Ser Glu Ser Gly Asn Ala Ile Phe Asn His Asp Gly Val  
 225 230 235 240  
 15 Asp Lys Leu Ser Phe Thr Gly Ser Thr Asp Val Gly Tyr Gln Val Ala  
 245 250 255  
 Glu Ala Ala Ala Lys His Leu Val Pro Ala Thr Leu Glu Leu Gly Gly  
 260 265 270  
 20 Lys Ser Ala Asn Ile Ile Leu Asp Asp Ala Asn Leu Asp Leu Ala Val  
 275 280 285  
 Glu Gly Ile Gln Leu Gly Ile Leu Phe Asn Gln Gly Glu Val Cys Ser  
 290 295 300  
 25 Ala Gly Ser Arg Leu Leu Val His Glu Lys Ile Tyr Asp Gln Leu Val  
 305 310 315 320  
 Pro Arg Leu Gln Glu Ala Phe Ser Asn Ile Lys Val Gly Asn Pro Gln  
 325 330 335  
 30 Asp Glu Ala Thr Gln Met Gly Ser Gln Thr Gly Lys Asp Gln Leu Asp  
 340 345 350  
 35 Lys Ile Gln Ser Tyr Ile Asp Ala Ala Lys Glu Ser Asp Ala Gln Ile  
 355 360 365  
 Leu Ala Gly Gly His Arg Leu Thr Glu Asn Gly Leu Asp Lys Gly Phe  
 370 375 380  
 40 Phe Phe Glu Pro Thr Leu Ile Ala Val Pro Asp Asn His His Lys Leu  
 385 390 395 400  
 Ala Gln Glu Glu Ile Phe Gly Pro Val Leu Thr Val Ile Lys Val Lys  
 405 410 415  
 45 Asp Asp Gln Glu Ala Ile Asp Ile Ala Asn Asp Ser Glu Tyr Gly Leu  
 420 425 430  
 Ala Gly Gly Val Phe Ser Gln Asn Ile Thr Arg Ala Leu Asn Ile Ala  
 435 440 445  
 50 Lys Ala Val Arg Thr Gly Arg Ile Trp Ile Asn Thr Tyr Asn Gln Val  
 450 455 460  
 55 Pro Glu Gly Ala Pro Phe Gly Gly Tyr Lys Lys Ser Gly Ile Gly Arg  
 465 470 475 480

Glu Thr Tyr Lys Gly Ala Leu Ser Asn Tyr Gln Gln Val Lys Asn Ile  
 485 490 495

Tyr Ile Asp Thr Ser Asn Ala Leu Lys Gly Leu Tyr  
 500 505

5

## (2) INFORMATION FOR SEQ ID NO:5242:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

10

## (ii) MOLECULE TYPE: protein

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5242:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn  
 1 5 10 15

Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile  
 20 25 30

25

Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr  
 35 40 45

Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala  
 50 55 60

30

Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln  
 65 70 75 80

Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro  
 85 90 95

35

Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly  
 100 105 110

Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp  
 115 120 125

40

Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala  
 130 135 140

Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala  
 145 150 155 160

45

Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln  
 165 170 175

50

Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala  
 180 185 190

Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp  
 195 200 205

55

Pro Ala Ile Ser Thr Asp Glu Asn Arg Gln Asp Pro Thr Val Thr Val  
 210 215 220  
 5 Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly  
 225 230 235 240  
 Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn  
 245 250  
 10 Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val  
 260 265 270  
 Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys  
 275 280 285  
 15 Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr  
 290 295 300  
 Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp  
 305 310 315 320  
 20 Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly  
 325 330 335  
 Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu  
 340 345 350  
 25 Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr  
 355 360 365  
 Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly  
 370 375 380  
 30 Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro  
 385 390 395 400  
 35 Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn  
 405 410 415  
 Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu  
 420 425 430  
 40 Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr  
 435 440 445  
 Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr  
 450 455 460  
 45 Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly  
 465 470 475 480  
 Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp  
 485 490 495  
 50 Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr  
 500 505 510  
 55 Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser  
 515 520 525

Asp Val Val Ile Asn Asn Ala Gln Pro Glu Val His  
 530 535 540

## (2) INFORMATION FOR SEQ ID NO:5243:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 274 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5243:

Ile Thr Leu Lys Thr Val Ser Gln Leu Ile Asp Met Lys Gln Lys Gln  
 1 5 10 15  
 Thr Lys Ile Ser Met Val Thr Ala Tyr Asp Phe Pro Ser Ala Lys Gln  
 20 25 30  
 Val Glu Ala Ala Gly Ile Asp Met Ile Leu Val Gly Asp Ser Leu Gly  
 35 40 45  
 Met Thr Val Leu Gly Tyr Glu Ser Thr Val Gln Val Thr Leu Ala Asp  
 50 55 60  
 Met Ile His His Gly Arg Ala Val Arg Arg Gly Ala Pro Asn Thr Phe  
 65 70 75 80  
 Val Val Val Asp Met Pro Ile Gly Ala Val Gly Ile Ser Met Thr Gln  
 85 90 95  
 Asp Leu Asn His Ala Leu Lys Leu Tyr Gln Glu Thr Asn Ala Asn Ala  
 100 105 110  
 Ile Lys Ala Glu Gly Ala His Ile Thr Pro Phe Ile Glu Lys Ala Thr  
 115 120 125  
 Ala Ile Gly Ile Pro Val Val Ala His Leu Gly Leu Thr Pro Gln Ser  
 130 135 140  
 Val Gly Val Met Gly Tyr Lys Leu Gln Gly Ala Thr Lys Glu Ala Ala  
 145 150 155 160  
 Glu Gln Leu Ile Leu Asp Ala Lys Asn Val Glu Gln Ala Gly Ala Val  
 165 170 175  
 Ala Leu Val Leu Glu Ala Ile Pro Asn Asp Leu Ala Glu Glu Ile Ser  
 180 185 190  
 Lys His Leu Thr Ile Pro Val Ile Gly Ile Gly Ala Gly Lys Gly Thr  
 195 200 205  
 Asp Gly Gln Val Leu Val Tyr His Asp Met Leu Asn Tyr Gly Val Glu  
 210 215 220

His Lys Ala Lys Phe Val Lys Gln Phe Ala Asp Phe Ser Val Gly Val  
 225 230 235 240

Asp Gly Leu Lys Gln Tyr Asp Gln Glu Val Lys Ser Gly Ala Phe Pro  
 245 250 255

Ser Glu Glu Tyr Thr Tyr Lys Lys Lys Ile Met Asn Glu Val Asn Asn  
 260 265 270

Asn Asp

## (2) INFORMATION FOR SEQ ID NO:5244:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 430 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5244:

Ser Asp Asp Trp Pro Lys Ser Ile Thr Ser Leu Ser Ile Arg Gly Val  
 1 5 10 15

Arg Met Lys His Gln Glu Thr Thr Ser Gln Gln Tyr Asn Phe Ser Ile  
 20 25 30

Ile Lys His Gly Asp Ile Ser Thr Pro Gln Gly Phe Thr Ala Gly Gly  
 35 40 45

Met His Ile Gly Leu Arg Ala Asn Lys Lys Asp Phe Gly Trp Ile Tyr  
 50 55 60

Ser Ser Ser Leu Ala Ser Ala Ala Ala Val Tyr Thr Leu Asn Gln Phe  
 65 70 75 80

Lys Ala Ala Pro Leu Ile Val Thr Glu Asp Thr Leu Gln Lys Ser Lys  
 85 90 95

Gly Lys Leu Gln Ala Leu Val Val Asn Ser Ala Asn Ala Asn Ser Cys  
 100 105 110

Thr Gly Gln Gln Gly Ile Asp Asp Ala Arg Gln Thr Gln Thr Trp Val  
 115 120 125

Ala Gln Gln Leu Gln Ile Pro Ser Glu His Val Ala Val Ala Ser Thr  
 130 135 140

Gly Val Ile Gly Glu Tyr Leu Pro Met Asp Lys Ile Lys Thr Gly Thr  
 145 150 155 160

Glu His Ile Lys Asp Ala Asn Phe Ala Thr Pro Gly Ala Phe Asn Glu  
 165 170 175

Ala Ile Leu Thr Thr Asp Thr Cys Thr Lys His Ile Ala Val Ser Leu  
180 185 190

5 Lys Ile Asp Gly Lys Thr Val Thr Ile Gly Gly Ser Thr Lys Gly Ser  
195 200 205

Gly Met Ile His Pro Asn Met Ala Thr Met Leu Ala Phe Ile Thr Thr  
210 215 220

10 Asp Ala Ser Ile Glu Ser Asn Thr Leu His Gln Leu Leu Lys Ser Ser  
225 230 235 240

Thr Asp His Thr Phe Asn Met Ile Thr Val Asp Gly Asp Thr Ser Thr  
245 250 255

15 Asn Asp Met Val Leu Val Met Ala Asn His Gln Val Glu His Gln Ile  
260 265 270

20 Leu Ser Gln Asp His Pro Gln Trp Glu Thr Phe Val Asp Ala Phe Asn  
275 280 285

Phe Val Cys Thr Phe Leu Ala Lys Ala Ile Ala Arg Asp Gly Glu Gly  
290 295 300

25 Ala Thr Lys Leu Ile Ser Val Asn Val Ser Gly Ala Lys Ser Ile Ser  
305 310 315 320

Asp Ala Arg Lys Ile Gly Lys Thr Ile Val Ser Ser Asn Leu Val Lys  
325 330 335

30 Ser Ala Ile Phe Gly Glu Asp Ala Asn Phe Gly Arg Ile Ile Thr Ala  
340 345 350

Ile Gly Tyr Ser Gly Cys Glu Ile Asp Pro Asn Cys Thr Tyr Val Gln  
355 360 365

35 Leu Asn Gln Ile Pro Val Val Asp Lys Gly Met Ala Val Leu Phe Asp  
370 375 380

40 Glu Gln Ala Met Ser Asn Thr Leu Thr His Glu Asn Val Thr Ile Asp  
385 390 395 400

Val Gln Leu Gly Leu Gly Asn Ala Ala Ala Thr Ala Tyr Gly Cys Asp  
405 410 415

45 Leu Ser Tyr Asp Tyr Val Arg Ile Asn Ala Ser Tyr Arg Thr  
420 425 430

## (2) INFORMATION FOR SEQ ID NO:5245:

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 469 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5245:

5 Asn Pro Ala Leu Thr Val Phe Ala Phe Ile Met Ile Ile Ser Ile Leu  
 1 5 10 15  
 Leu Ala Tyr Val Phe Lys Trp Leu Gly Leu Val Asp Asp Val Leu Leu  
 20 25 30  
 10 Met Val Ile Ile Ile Ser Thr Ile Ser Leu Gly Val Val Val Pro Thr  
 35 40 45  
 Leu Lys Glu Met Asn Ile Met Arg Thr Thr Ile Gly Gln Phe Ile Leu  
 50 55 60  
 15 Leu Val Ala Val Leu Ala Asp Leu Val Thr Met Ile Leu Leu Thr Val  
 65 70 75 80  
 Tyr Gly Ala Ile Asn Gly Gln Gly Gly Ser Thr Ile Trp Leu Ile Gly  
 85 90 95  
 20 Ile Leu Val Val Phe Thr Ala Ile Ser Tyr Ile Leu Gly Val Gln Phe  
 100 105 110  
 Lys Arg Met Ser Phe Leu Gln Lys Leu Met Asp Gly Thr Thr Gln Ile  
 115 120 125  
 25 Gly Ile Arg Ala Val Phe Ala Leu Ile Ile Leu Leu Val Ala Leu Ala  
 130 135 140  
 Glu Gly Val Gly Ala Glu Asn Ile Leu Gly Ala Phe Leu Ala Gly Val  
 145 150 155 160  
 30 Val Val Ser Leu Leu Asn Pro Asp Glu Glu Met Val Glu Lys Leu Asp  
 165 170 175  
 35 Ser Phe Gly Tyr Gly Phe Phe Ile Pro Ile Phe Phe Ile Met Xaa Gly  
 180 185 190  
 Val Asp Leu Asn Ile Pro Ser Leu Ile Lys Glu Pro Lys Leu Leu Ile  
 195 200 205  
 40 Ile Ile Pro Ile Leu Ile Val Ala Phe Ile Ile Ser Lys Leu Ile Pro  
 210 215 220  
 Val Met Phe Ile Arg Arg Trp Phe Asp Met Lys Thr Thr Ile Ala Ser  
 225 230 235 240  
 45 Ala Phe Leu Leu Thr Ser Thr Leu Ser Leu Val Ile Ala Ala Ala Lys  
 245 250 255  
 50 Ile Ser Glu Arg Leu Asn Ala Ile Ser Ala Glu Thr Ser Gly Ile Leu  
 260 265 270  
 Ile Leu Ser Ala Val Ile Thr Cys Val Phe Val Pro Ile Ile Phe Lys  
 275 280 285  
 55 Lys Leu Phe Pro Val Pro Asp Glu Phe Asn Arg Lys Ile Glu Val Ser  
 290 295 300



Leu Ile Gly Lys Asn Gln Leu Thr Ile Pro Ile Ala Gln Asn Leu Thr  
 305 310 315 320  
 5 Ser Gln Leu Tyr Asp Val Thr Leu Tyr Tyr Arg Lys Asp Leu Ser Asp  
 325 330 335  
 Arg Arg Gln Leu Ser Asp Asp Ile Thr Met Ile Glu Ile Ala Asp Tyr  
 340 345 350  
 10 Glu Gln Asp Val Leu Glu Arg Leu Gly Leu Phe Asp Arg Asp Ile Val  
 355 360 365  
 Val Cys Ala Thr Asn Asp Asp Asp Ile Asn Arg Lys Val Ala Lys Leu  
 370 375 380  
 15 Ala Lys Ala His Gln Val Glu Arg Val Ile Cys Arg Leu Glu Ser Thr  
 385 390 395 400  
 Thr Asp Asp Thr Glu Leu Val Asp Ser Gly Ile Glu Ile Phe Ser Ser  
 405 410 415  
 20 Tyr Leu Ser Asn Lys Ile Leu Leu Lys Gly Leu Ile Glu Thr Pro Asn  
 420 425 430  
 Met Leu Asn Leu Leu Ser Asn Val Glu Thr Ser Leu Tyr Glu Ile Gln  
 435 440 445  
 25 Met Leu Asn Tyr Lys Tyr Glu Asn Ile Gln Leu Arg Asn Phe Pro Phe  
 450 455 460  
 30 Gly Gly Asp Ile Ile  
 465

## (2) INFORMATION FOR SEQ ID NO:5246:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 414 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5246:  
 Ala Ile Ile Val Ile Leu Leu Phe Leu Arg Asn Ile Arg Thr Thr Ala  
 1 5 10 15  
 Ile Ser Ile Ile Ser Ile Pro Leu Ser Leu Leu Met Ala Leu Ile Ala  
 20 25 30  
 50 Leu Lys Leu Ser Asp Val Ser Leu Asn Ile Leu Thr Leu Gly Ala Leu  
 35 40 45  
 55 Thr Val Ala Ile Gly Arg Val Ile Asp Asp Ser Ile Val Val Val Glu  
 50 55 60

Asn Ile Tyr Arg Arg Leu Thr Asp Ser Glu Glu Gln Leu Lys Gly Glu  
 65 70 75 80  
 5 Asn Leu Ile Ile Ser Ala Thr Thr Glu Val Phe Lys Pro Ile Met Ser  
 85 90 95  
 Ser Thr Leu Val Thr Ile Ile Val Phe Leu Pro Leu Val Phe Val Ser  
 100 105 110  
 10 Gly Ser Val Gly Glu Met Phe Arg Pro Phe Ala Leu Ala Ile Ala Phe  
 115 120 125  
 Ser Leu Leu Ala Ser Leu Leu Val Ser Ile Thr Leu Val Pro Ala Leu  
 130 135 140  
 15 Ala Ala Thr Leu Phe Lys Lys Gly Val Lys Arg Arg Asn Lys Gln His  
 145 150 155 160  
 Gln Glu Gly Leu Gly Val Val Ser Thr Thr Tyr Lys Lys Val Leu His  
 165 170 175  
 20 Trp Ser Leu Asn His Lys Trp Ile Val Ile Ile Leu Ser Thr Leu Ile  
 180 185 190  
 Leu Val Ala Thr Ile Val Phe Gly Gly Pro Arg Leu Gly Thr Ser Phe  
 195 200 205  
 25 Ile Ser Ala Gly Asp Asp Lys Phe Leu Ala Ile Thr Tyr Thr Pro Lys  
 210 215 220  
 Pro Gly Glu Thr Glu Gln Ala Val Leu Asn His Ala Lys Asp Val Glu  
 225 230 235 240  
 Lys Tyr Leu Lys Gln Lys Lys His Val Lys Thr Ile Gln Tyr Ser Val  
 245 250 255  
 35 Gly Gly Ser Ser Pro Val Asp Pro Thr Gly Ser Thr Asn Ser Met Ala  
 260 265 270  
 Ile Met Val Glu Tyr Asp Asn Asp Thr Pro Asn Phe Asp Val Glu Ala  
 275 280 285  
 40 Asp Lys Val Ile Lys His Ala Asp Gly Phe Lys His Pro Gly Glu Trp  
 290 295 300  
 Lys Asn Gln Asp Leu Gly Thr Gly Ala Gly Asn Lys Ser Val Glu Val  
 305 310 315 320  
 45 Thr Val Lys Gly Pro Ser Met Asp Ala Ile Lys Ser Thr Val Lys Asp  
 325 330 335  
 Ile Glu Gln Lys Met Lys Gln Val Lys Gly Leu Ala Asn Val Lys Ser  
 340 345 350  
 50 Asp Leu Ser Gln Thr Tyr Asp Gln Tyr Glu Ile Lys Val Asp Gln Asn  
 355 360 365  
 55 Lys Ala Ala Glu Asn Gly Ile Ser Ala Ser Gln Leu Ala Met His Leu  
 370 375 380

Asn Glu Asn Leu Pro Glu Lys Thr Val Thr Thr Val Lys Glu Asn Gly  
 385 390 395 400

Lys Thr Val Asp Val Lys Val Lys Gln Asn Lys Gln Thr Ala  
 405 410

(2) INFORMATION FOR SEQ ID NO:5247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5247:

Gly Lys Pro Phe Ile Ile Gly Leu Gly Asp Ile Ile Val Lys Lys Leu  
 1 5 10 15  
 Thr Thr Ile Leu Phe Gln Tyr Lys Ile Phe Pro Val Leu Met Phe Leu  
 20 25 30  
 Val Ser Thr Gly Leu Gly Ile Ile Val Ile Thr Gln Asn Ile Leu Ile  
 35 40 45  
 Ala Asp Phe Leu Ala Lys Ile Ile Arg His Gln Phe Gln Gly Leu Trp  
 50 55 60  
 Ile Val Leu Phe Ile Leu Leu Gly Val Leu Leu Leu Arg Ala Thr Val  
 65 70 75 80  
 Gln Phe Leu Asn Gln Trp Leu Gly Asp Thr Leu Ala Phe Lys Val Lys  
 85 90 95  
 His Met Leu Arg Gln Arg Val Ile Tyr Lys Asn Asn Gly His Pro Ile  
 100 105 110  
 Gly Glu Gln Met Thr Ile Leu Thr Glu Asn Ile Asp Gly Leu Ala Pro  
 115 120 125  
 Phe Tyr Lys Ser Tyr Leu Pro Gln Val Phe Lys Ser Met Met Val Pro  
 130 135 140  
 Leu Ile Ile Ile Ile Ala Met Phe Phe Ile His Phe Asn Thr Ala Leu  
 145 150 155 160  
 Ile Met Leu Ile Thr Ala Pro Phe Ile Pro Leu Phe Tyr Ile Ile Phe  
 165 170 175  
 Gly Leu Lys Thr Arg Asp Glu Ser Lys Asp Gln Met Thr Tyr Leu Asn  
 180 185 190  
 Gln Phe Ser Gln Arg Phe Leu Asn Ile Ala Lys Gly Leu Val Thr Leu  
 195 200 205

Lys Leu Phe Asn Arg Thr Glu Gln Thr Glu Lys His Ile Tyr Asp Asp  
 210 215 220  
 Ser Thr Gln Phe Arg Thr Leu Thr Met Arg Ile Leu Arg Ser Ala Phe  
 225 230 240  
 Leu Ser Gly Leu Met Leu Glu Phe Ile Ser Met Leu Gly Ile Gly Leu  
 245 250 255  
 Val Ala Leu Glu Ala Thr Leu Ser Leu Val Val Phe His Asn Ile Asp  
 260 265 270  
 Phe Lys Thr Ala Ala Ile Ala Ile Ile Leu Ala Pro Glu Phe Tyr Asn  
 275 280 285  
 Ala Ile Lys Asp Leu Gly Gln Ala Phe His Thr Gly Lys Gln Ser Glu  
 290 295 300  
 Gly Ala Ser Asp Val Val Phe Glu Phe Leu Glu Gln Pro Asn Tyr Asn  
 305 310 315 320  
 Asn Glu Phe Leu Leu Lys Tyr Glu Glu Asn Gln Lys Pro Phe Ile Gln  
 325 330 335  
 Leu Thr Asp Ile Ser Phe Arg Tyr Asp Asp Ser Asp Arg Leu Val Leu  
 340 345 350  
 Asn Asp Leu Asn Leu Glu Ile Phe Lys Gly Asp Gln Ile Ala Leu Val  
 355 360 365  
 Gly Pro Ser Gly Ala Gly Lys Ser Thr Leu Thr His Leu Ile Ala Gly  
 370 375 380  
 Val Tyr Gln Pro Thr Ile Gly Thr Ile Ser Thr Asn Gln Arg Asp Leu  
 385 390 395 400  
 Asn Ile Gly Ile Leu Ser Gln Gln Pro Tyr Ile Phe Ser Ala Ser Ile  
 405 410 415  
 Lys Glu Asn Ile Thr Met Phe Lys Asp Ile Glu Asn Asn Thr Ile Glu  
 420 425 430  
 Glu Val Leu Asp Glu Val Gly Leu Leu Asp Lys Val Gln Ser Phe Thr  
 435 440 445  
 Lys Gly Ile Asn Thr Ile Ile Gly Glu Gly Gly Glu Met Leu Ser Gly  
 450 455 460  
 Gly Gln Met Arg Arg Ile Glu Leu Cys Arg Leu Leu Val Met Lys Pro  
 465 470 475 480  
 Asp Leu Val Ile Phe Asp Glu Pro Ala Thr Gly Leu Asp Ile Gln Thr  
 485 490 495  
 Glu His Met Ile Gln Asn Val Leu Phe Gln His Phe Lys Asp Thr Thr  
 500 505 510  
 Met Ile Val Ile Ala His Arg Asp Asn Thr Ile Arg His Leu Gln Arg  
 515 520 525

Arg Leu Tyr Ile Glu Asn Gly Arg Leu Ile Ala Asp Asp Arg Asn Ile  
 530 535 540

Ser Val Asn Ile Thr Glu Asn Gly Asp Asp Leu  
 545 550 555

## (2) INFORMATION FOR SEQ ID NO:5248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5248:

Val Trp Lys Leu Lys Met Arg Trp Ile Lys Arg Lys Lys Lys Asn Phe  
 1 5 10 15  
 Leu Asn Ser Lys Phe Asn Phe Asn Asn Gly Lys Ile Ala Thr Tyr Leu  
 20 25 30  
 Tyr Lys Glu Arg Thr Ala Met Trp Asn Lys Asn Arg Leu Thr Gln Met  
 35 40 45  
 Leu Ser Ile Glu Tyr Pro Ile Ile Gln Ala Gly Met Ala Gly Ser Thr  
 50 55 60  
 Thr Pro Lys Leu Val Ala Ser Val Ser Asn Ser Gly Gly Leu Gly Thr  
 65 70 75 80  
 Ile Gly Ala Gly Tyr Phe Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp  
 85 90 95  
 Tyr Val Arg Gln Leu Thr Ser Asn Ser Phe Gly Val Asn Val Phe Val  
 100 105 110  
 Pro Ser Gln Gln Ser Tyr Thr Ser Ser Gln Ile Glu Asn Met Asn Ala  
 115 120 125  
 Trp Leu Lys Pro Tyr Arg Arg Ala Leu His Leu Glu Glu Pro Val Val  
 130 135 140  
 Lys Ile Thr Glu Glu Gln Gln Phe Lys Cys His Ile Asp Thr Ile Ile  
 145 150 155 160  
 Lys Lys Gln Val Pro Val Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu  
 165 170 175  
 Gln Ile Ile Ser Arg Leu Lys Ala Ala Asn Val Lys Leu Ile Gly Thr  
 180 185 190  
 Ala Thr Ser Val Asp Glu Ala Ile Ala Asn Glu Lys Ala Gly Met Asp  
 195 200 205

Ala Ile Val Ala Gln Gly Ser Glu Ala Gly Gly His Arg Gly Ser Phe  
 210 215 220  
 5 Leu Lys Pro Lys Asn Gln Leu Pro Met Val Gly Thr Ile Ser Leu Val  
 225 230 235 240  
 Pro Gln Ile Val Asp Val Val Ser Ile Pro Val Ile Ala Ala Gly Gly  
 245 250 255  
 10 Ile Met Asp Gly Arg Gly Val Leu Ala Ser Ile Val Leu Gly Ala Glu  
 260 265 270  
 Gly Val Gln Met Gly Thr Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala  
 275 280 285  
 15 Ser Glu Leu Leu Arg Asp Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr  
 290 295 300  
 Val Ile Thr Lys Ala Phe Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn  
 305 310 315 320  
 20 Arg Phe Ile Glu Glu Met Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr  
 325 330 335  
 Pro Ile Gln Asn Glu Leu Thr Ser Ser Ile Arg Lys Ala Ala Asn Asn  
 340 345 350  
 25 Ile Gly Asp Lys Glu Leu Ile His Met Trp Ser Gly Gln Ser Pro Arg  
 355 360 365  
 Leu Ala Thr Thr His Pro Ala Asn Thr Ile Met Ser Asn Ile Ile Asn  
 370 375 380  
 30 Gln Ile Asn Gln Ile Met Gln Tyr Lys  
 385 390

## (2) INFORMATION FOR SEQ ID NO:5249:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 936 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5249:

Asn Asp Phe Leu Lys Arg Gly Asn Lys Met Asn Met Lys Lys Lys Glu  
 1 5 10  
 50 Lys His Ala Ile Arg Lys Lys Ser Ile Gly Val Ala Ser Val Leu Val  
 20 25 30  
 Gly Thr Leu Ile Gly Phe Gly Leu Leu Ser Ser Lys Glu Ala Asp Ala  
 35 40 45

|    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|    | Ser | Glu | Asn | Ser | Val | Thr | Gln | Ser | Asp | Ser | Ala | Ser | Asn | Glu | Ser | Lys |
|    | 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| 5  | Ser | Asn | Asp | Ser | Ser | Ser | Val | Ser | Ala | Ala | Pro | Lys | Thr | Asp | Asp | Thr |
|    | 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |
|    | Asn | Val | Ser | Asp | Thr | Lys | Thr | Ser | Ser | Asn | Thr | Asn | Asn | Gly | Glu | Thr |
|    |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| 10 | Ser | Val | Ala | Gln | Asn | Pro | Ala | Gln | Gln | Glu | Thr | Thr | Gln | Ser | Ser | Ser |
|    |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
|    | Thr | Asn | Ala | Thr | Thr | Glu | Glu | Thr | Pro | Val | Thr | Gly | Glu | Ala | Thr | Thr |
|    |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| 15 | Thr | Thr | Thr | Asn | Gln | Ala | Asn | Thr | Pro | Ala | Thr | Thr | Gln | Ser | Ser | Asn |
|    |     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
|    | Thr | Asn | Ala | Glu | Glu | Leu | Val | Asn | Gln | Thr | Ser | Asn | Glu | Thr | Thr | Ser |
|    |     |     |     |     | 145 |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| 20 | Asn | Asp | Thr | Asn | Thr | Val | Ser | Ser | Val | Asn | Ser | Pro | Gln | Asn | Ser | Thr |
|    |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
|    | Asn | Ala | Glu | Asn | Val | Ser | Thr | Thr | Gln | Asp | Thr | Ser | Thr | Glu | Ala | Thr |
|    |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| 25 | Pro | Ser | Asn | Asn | Glu | Ser | Ala | Pro | Gln | Ser | Thr | Asp | Ala | Ser | Asn | Lys |
|    |     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| 30 | Asp | Val | Val | Asn | Gln | Ala | Val | Asn | Thr | Ser | Ala | Pro | Arg | Met | Arg | Ala |
|    |     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
|    | Phe | Ser | Leu | Ala | Ala | Val | Ala | Ala | Asp | Ala | Pro | Val | Ala | Gly | Thr | Asp |
|    |     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |
| 35 | Ile | Thr | Asn | Gln | Leu | Thr | Asn | Val | Thr | Val | Gly | Ile | Asp | Ser | Gly | Thr |
|    |     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
|    | Thr | Val | Tyr | Pro | His | Gln | Ala | Gly | Tyr | Val | Lys | Leu | Asn | Tyr | Gly | Phe |
|    |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| 40 | Ser | Val | Pro | Asn | Ser | Ala | Val | Lys | Gly | Asp | Thr | Phe | Lys | Ile | Thr | Val |
|    |     |     |     |     | 275 |     |     | 280 |     |     |     |     | 285 |     |     |     |
|    | Pro | Lys | Glu | Leu | Asn | Leu | Asn | Gly | Val | Thr | Ser | Thr | Ala | Lys | Val | Pro |
|    |     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| 45 | Pro | Ile | Met | Ala | Gly | Asp | Gln | Val | Leu | Ala | Asn | Gly | Val | Ile | Asp | Ser |
|    |     |     |     |     | 305 |     | 310 |     |     |     | 315 |     |     |     |     | 320 |
|    | Asp | Gly | Asn | Val | Ile | Tyr | Thr | Phe | Thr | Asp | Tyr | Val | Asn | Thr | Lys | Asp |
|    |     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| 50 | Asp | Val | Lys | Ala | Thr | Leu | Thr | Met | Pro | Ala | Tyr | Ile | Asp | Pro | Glu | Asn |
|    |     |     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |
| 55 | Val | Lys | Lys | Thr | Gly | Asn | Val | Thr | Leu | Ala | Thr | Gly | Ile | Gly | Ser | Thr |
|    |     |     |     |     | 355 |     |     | 360 |     |     |     |     |     | 365 |     |     |

Thr Ala Asn Lys Thr Val Leu Val Asp Tyr Glu Lys Tyr Gly Lys Phe  
 370 375 380  
 Tyr Asn Leu Ser Ile Lys Gly Thr Ile Asp Gln Ile Asp Lys Thr Asn  
 5 385 390 395 400  
 Asn Thr Tyr Arg Gln Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val  
 405 415  
 Ile Ala Pro Val Leu Thr Gly Asn Leu Lys Pro Asn Thr Asp Ser Asn  
 10 420 425 430  
 Ala Leu Ile Asp Gln Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp  
 435 440 445  
 Asn Ala Ala Asp Leu Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe  
 15 450 455 460  
 Glu Asp Val Thr Asn Ser Val Asn Ile Thr Phe Pro Asn Pro Asn Gln  
 465 470 475 480  
 Tyr Lys Val Glu Phe Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr  
 20 485 490 495  
 Ile Val Val Val Asn Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu  
 25 500 505 510  
 Ala Leu Arg Ser Thr Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg  
 515 520 525  
 Ser Met Ser Trp Asp Asn Glu Val Ala Phe Asn Asn Gly Ser Gly Ser  
 30 530 535 540  
 Gly Asp Gly Ile Asp Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro  
 545 550 555 560  
 Gly Glu Ile Glu Pro Ile Pro Glu Asp Ser Asp Ser Asp Pro Gly Ser  
 35 565 570 575  
 Asp Ser Gly Ser Asp Ser Asn Ser Asp Ser Gly Ser Asp Ser Gly Ser  
 580 585 590  
 Asp Ser Thr Ser Asp Ser Gly Ser Asp Ser Ala Ser Asp Ser Asp Ser  
 40 595 600 605  
 Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser  
 610 615 620  
 Asp Ser Ala Ser Asp Ser Asp Ser Asp Asn Asp Ser Asp Ser Asp Ser  
 45 625 630 635 640  
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 645 650 655  
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 50 660 665 670  
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 55 675 680 685



Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 690 695 700  
 5 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 705 710 715 720  
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 725 730 735  
 10 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 740 745 750  
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 755 760 765  
 15 Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Asp Ser  
 770 775 780  
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 785 790 795 800  
 20 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 805 810 815  
 25 Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 820 825 830  
 Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Gly Ser  
 835 840 845  
 30 Asp Ser Asp Ser Ser Ser Asp Ser Asp Ser Glu Ser Asp Ser Asn Ser  
 850 855 860  
 Asp Ser Glu Ser Val Ser Asn Asn Asn Val Val Pro Pro Asn Ser Pro  
 865 870 875 880  
 35 Lys Asn Gly Thr Asn Ala Ser Asn Lys Asn Glu Ala Lys Asp Ser Lys  
 885 890 895  
 40 Glu Pro Leu Pro Asp Thr Gly Ser Glu Asp Glu Ala Asn Thr Ser Leu  
 900 905 910  
 Ile Trp Gly Leu Leu Ala Ser Ile Gly Ser Leu Leu Leu Phe Arg Arg  
 915 920 925  
 45 Lys Lys Glu Asn Lys Asp Lys Lys  
 930 935

## (2) INFORMATION FOR SEQ ID NO:5250:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 194 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5250:

Val Ser Lys Leu Lys Lys Glu Ile Leu Glu Trp Ile Ile Ser Ile Ala  
 1 5 10 15  
 Val Ala Phe Val Val Ile Leu Phe Ile Val Gly Lys Phe Ile Val Thr Pro  
 20 25 30  
 Tyr Thr Ile Lys Gly Glu Ser Met Asp Pro Thr Leu Lys Asp Gly Glu  
 35 40 45  
 Arg Val Ala Val Asn Ile Val Gly Tyr Lys Thr Gly Gly Leu Glu Lys  
 50 55 60  
 Gly Asn Val Val Val Phe His Ala Asn Lys Asn Asp Asp Tyr Val Lys  
 65 70 75 80  
 Arg Val Ile Gly Val Pro Gly Asp Lys Val Glu Tyr Lys Asn Asp Thr  
 85 90 95  
 Leu Tyr Val Asn Gly Lys Lys Gln Asp Glu Pro Tyr Leu Asn Tyr Asn  
 100 105 110  
 Leu Lys His Lys Lys Gln Gly Asp Tyr Ile Thr Gly Thr Phe Gln Val Lys  
 115 120 125  
 Asp Leu Pro Asn Ala Asn Pro Lys Ser Asn Val Ile Pro Lys Gly Lys  
 130 135 140  
 Tyr Leu Val Leu Gly Asp Asn Arg Glu Val Ser Lys Asp Ser Arg Ala  
 145 150 155 160  
 Phe Gly Leu Ile Asp Glu Asp Gln Ile Val Gly Lys Val Ser Phe Gln  
 165 170 175  
 Val Leu Ala His Phe Ser Glu Phe Gln Thr Ser Ile Ser Xaa Leu Lys  
 180 185 190  
 Ile Leu

(2) INFORMATION FOR SEQ ID NO:5251:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 559 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5251:

Leu Lys Ala Xaa Tyr Ala Lys Leu Asp Asp Val Ser Lys Phe Glu Asp  
 1 5 10 15

Val Thr Asp Asn Met Ser Leu Asp Phe Asp Thr Asn Gly Gly Tyr Ser  
20 25 30

5 Leu Asn Phe Asn Asn Leu Asp Gln Ser Lys Asn Tyr Val Ile Lys Tyr  
35 40 45

Glu Gly Tyr Tyr Asp Ser Asn Ala Ser Asn Leu Glu Phe Gln Thr His  
50 55 60

10 Leu Phe Gly Tyr Tyr Asn Tyr Tyr Thr Ser Asn Leu Thr Trp Lys  
65 70 75 80

Asn Gly Val Ala Phe Tyr Ser Asn Asn Ala Gln Gly Asp Gly Lys Asp  
85 90 95

15 Lys Leu Lys Glu Pro Ile Ile Glu His Ser Thr Pro Ile Glu Leu Glu  
100 105 110

Phe Lys Ser Glu Pro Pro Val Glu Lys His Glu Leu Thr Gly Thr Ile  
115 120 125

20 Glu Glu Ser Asn Asp Ser Lys Pro Ile Asp Phe Glu Tyr His Thr Ala  
130 135 140

25 Val Glu Gly Ala Glu Gly His Ala Glu Gly Thr Ile Glu Thr Glu Glu  
145 150 155 160

Asp Ser Ile His Val Asp Phe Glu Glu Ser Thr His Glu Asn Ser Lys  
165 170 175

30 His His Ala Asp Val Val Glu Tyr Glu Glu Asp Thr Asn Pro Gly Gly  
180 185 190

Gly Gln Val Thr Thr Glu Ser Asn Leu Val Glu Phe Asp Glu Asp Ser  
195 200 205

35 Thr Lys Gly Ile Val Thr Gly Ala Val Ser Asp His Thr Thr Ile Glu  
210 215 220

Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn Leu Ile Glu Leu Val Asp  
225 230 235 240

40 Glu Leu Pro Glu Glu His Gly Gln Ala Gln Gly Pro Ile Glu Glu Ile  
245 250 255

Thr Glu Asn Asn His His Ile Ser His Ser Gly Leu Gly Thr Glu Asn  
260 265 270

45 Gly His Gly Asn Tyr Gly Val Ile Glu Ile Glu Glu Asn Ser His  
275 280 285

50 Val Asp Ile Lys Ser Glu Leu Glu Tyr Glu Gly Gly Gln Asn Ser Gly  
290 295 300

Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu Asp Lys Pro Lys Tyr Glu  
305 310 315 320

55 Gln Gly Gly Asn Ile Val Asp Ile Asp Phe Asp Ser Val Pro Gln Ile  
325 330 335

His Gly Gln Asn Asn Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Lys  
 340 345 350  
 5 Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Ile Asp Ile Asp Phe  
 355 360 365  
 Asp Ser Val Pro His Ile His Gly Phe Asn Lys His Thr Glu Ile Ile  
 370 375 380  
 10 Glu Glu Asp Thr Asn Lys Asp Lys Pro Asn Tyr Gln Phe Gly Gly His  
 385 390 395 400  
 Asn Ser Val Asp Phe Glu Glu Asp Thr Leu Pro Gln Val Ser Gly His  
 405 410 415  
 15 Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro Ile Val  
 420 425 430  
 Pro Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro  
 435 440 445  
 20 Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro Thr Pro  
 450 455 460  
 Pro Thr Pro Glu Val Pro Thr Glu Pro Gly Lys Pro Ile Pro Pro Ala  
 465 470 475 480  
 25 Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu Gln Gly Lys Val  
 485 490 495  
 Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys Ala Val Val Pro  
 500 505 510  
 30 Thr Lys Lys Ala Gln Ser Lys Lys Ser Glu Leu Pro Glu Thr Gly Gly  
 515 520 525  
 Glu Glu Ser Thr Asn Asn Gly Met Leu Phe Gly Gly Leu Phe Ser Ile  
 530 535 540  
 35 Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn His Lys Ala  
 545 550 555

## (2) INFORMATION FOR SEQ ID NO:5252:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5252:

Thr Lys Asn Glu Lys Ile Asn Asp Val Thr Ala Val Ala Glu Lys Glu  
 1 5 10 15

Val Val Glu Glu Thr Lys Ala Thr Gly Thr Asp Val Thr Asn Lys Val  
 20 25 30  
 Glu Val Glu Glu Gly Ser Glu Ile Val Gly His Lys Gln Asp Thr Asn  
 35 40 45  
 Val Val Asn Pro His Asn Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp  
 50 55 60  
 Lys Phe Gly Glu Gly Ile Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu  
 65 70 75 80  
 Ser Asp Asn Val Glu Thr His Gly Ile Ser Thr Leu Arg Lys Val Pro  
 85 90 95  
 Glu Ile Lys Ser Thr Asp Gly Gln Val Met Ala Thr Gly Glu Ile Ile  
 100 105 110  
 Gly Glu Arg Lys Val Arg Tyr Thr Phe Lys Glu Tyr Val Gln Glu Lys  
 115 120 125  
 Lys Asp Leu Thr Ala Glu Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr  
 130 135 140  
 Thr Val Thr Gln Lys Gly Asn Gln Asn Val Glu Val Lys Leu Gly Glu  
 145 150 155 160  
 Thr Thr Val Ser Lys Ile Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg  
 165 170 175  
 Asp Asn Trp Gly Val Thr Ala Asn Gly Arg Ile Asp Thr Leu Asn Lys  
 180 185 190  
 Val Asp Gly Lys Phe Ser His Phe Ala Tyr Met Lys Pro Asn Asn Gln  
 195 200 205  
 Ser Leu Ser Ser Val Thr Val Thr Gly Gln Val Thr Lys Gly Asn Lys  
 210 215 220  
 Pro Gly Val Asn Asn Pro Thr Val Lys Val Tyr Lys His Ile Gly Ser  
 225 230 235 240  
 Asp Asp Leu Ala Glu Ser Xaa Xaa Cys Lys Ala  
 245 250

## (2) INFORMATION FOR SEQ ID NO:5253:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 163 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5253:

Ile Leu His Leu Arg Glu Asn Ile Ile Val Lys Ser Asn Leu Arg Tyr  
 1 5 10 15  
 Gly Ile Arg Lys His Lys Leu Gly Ala Ser Val Phe Leu Gly Thr  
 20 25 30  
 Met Ile Val Val Gly Met Gly Gln Glu Lys Glu Ala Ala Ser Glu  
 35 40 45  
 Gln Asn Asn Thr Thr Val Glu Glu Ser Gly Ser Ser Ala Thr Glu Ser  
 50 55 60  
 Lys Ala Ser Glu Thr Gln Thr Thr Thr Asn Asn Val Asn Thr Ile Asp  
 65 70 75 80  
 Glu Thr Gln Ser Tyr Ser Ala Thr Ser Thr Glu Gln Pro Ser Gln Ser  
 85 90 95  
 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Thr Val Gln Ala Pro Lys  
 100 105 110  
 Val Glu Thr Ser Arg Val Asp Leu Pro Ser Glu Lys Val Ala Asp Lys  
 115 120 125  
 Glu Thr Thr Gly Thr Gln Val Asp Ile Ala Gln Pro Ser Asn Val Ser  
 130 135 140  
 Glu Ile Lys Pro Arg Met Lys Arg Ser Met Thr Leu Gln Gln Leu Gln  
 145 150 155 160  
 Arg Lys Lys

## (2) INFORMATION FOR SEQ ID NO:5254:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1027 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5254:

Ile Leu His Leu Lys Gly Asp Ile Ile Val Lys Asn Asn Leu Arg Tyr  
 1 5 10 15  
 Gly Ile Arg Lys His Lys Leu Gly Ala Ser Val Phe Leu Gly Thr  
 20 25 30  
 Met Ile Val Val Gly Met Gly Gln Asp Lys Glu Ala Ala Ala Ser Glu  
 35 40 45  
 Gln Lys Thr Thr Thr Val Glu Glu Asn Gly Asn Ser Ala Thr Asp Asn  
 50 55 60

Lys Thr Ser Glu Thr Gln Thr Thr Ala Thr Asn Val Asn His Ile Glu  
 65 70 75 80  
 5 Glu Thr Gln Ser Tyr Asn Ala Thr Val Thr Glu Gln Pro Ser Asn Ala  
 85 90 95  
 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Ala Val Gln Ala Pro Gln  
 100 105 110  
 10 Thr Ala Gln Pro Ala Asn Ile Glu Thr Val Lys Glu Glu Val Val Lys  
 115 120 125  
 Glu Glu Ala Lys Pro Gln Val Lys Glu Thr Thr Gln Ser Gln Asp Asn  
 130 135 140  
 15 Ser Gly Asp Gln Arg Gln Val Asp Leu Thr Pro Lys Lys Ala Thr Gln  
 145 150 155 160  
 Asn Gln Val Ala Glu Thr Gln Val Glu Val Ala Gln Pro Arg Thr Ala  
 165 170 175  
 20 Ser Glu Ser Lys Pro Arg Val Thr Arg Ser Ala Asp Val Ala Glu Ala  
 180 185 190  
 25 Lys Glu Ala Ser Asn Ala Lys Val Glu Thr Gly Thr Asp Val Thr Ser  
 195 200 205  
 Lys Val Thr Val Glu Ile Gly Ser Ile Glu Gly His Asn Asn Thr Asn  
 210 215 220  
 30 Lys Val Glu Pro His Ala Gly Gln Arg Ala Val Leu Lys Tyr Lys Leu  
 225 230 235 240  
 Lys Phe Glu Asn Gly Leu His Gln Gly Asp Tyr Phe Asp Phe Thr Leu  
 245 250 255  
 35 Ser Asn Asn Val Asn Thr His Gly Val Ser Thr Ala Arg Lys Val Pro  
 260 265 270  
 Glu Ile Lys Asn Gly Ser Val Val Met Ala Thr Gly Glu Val Leu Glu  
 275 280 285  
 40 Gly Gly Lys Ile Arg Tyr Thr Phe Thr Asn Asp Ile Glu Asp Lys Val  
 290 295 300  
 Asp Val Thr Ala Glu Leu Glu Ile Asn Leu Phe Ile Asp Pro Lys Thr  
 305 310 315 320  
 45 Val Gln Thr Asn Gly Asn Gln Thr Ile Thr Ser Thr Leu Asn Glu Glu  
 325 330 335  
 Gln Thr Ser Lys Glu Leu Asp Val Lys Tyr Lys Asp Gly Ile Gly Asn  
 340 345 350  
 50 Tyr Tyr Ala Asn Leu Asn Gly Ser Ile Glu Thr Phe Asn Lys Ala Asn  
 355 360 365  
 55 Asn Arg Phe Ser His Val Ala Phe Ile Lys Pro Asn Asn Gly Lys Thr  
 370 375 380

|    |                                                                 |                 |
|----|-----------------------------------------------------------------|-----------------|
|    | Thr Ser Val Thr Val Thr Gly Thr Leu Met Lys Gly Ser Asn Gln Asn |                 |
|    | 385                                                             | 390 395 400     |
| 5  | Gly Asn Gln Pro Lys Val Arg Ile Phe Glu Tyr Leu Gly Asn Asn Glu | 405 410 415     |
|    | Asp Ile Ala Lys Ser Val Tyr Ala Asn Thr Thr Asp Thr Ser Lys Phe | 420 425 430     |
| 10 | Lys Glu Val Thr Ser Asn Met Ser Gly Asn Leu Asn Leu Gln Asn Asn | 435 440 445     |
|    | Gly Ser Tyr Ser Leu Asn Ile Glu Asn Leu Asp Lys Thr Tyr Val Val | 450 455 460     |
| 15 | His Tyr Asp Gly Glu Tyr Leu Asn Gly Thr Asp Glu Val Asp Phe Arg | 465 470 475 480 |
|    | Thr Gln Met Val Gly His Pro Glu Gln Leu Tyr Lys Tyr Tyr Tyr Asp | 485 490 495     |
| 20 | Arg Gly Tyr Thr Leu Thr Trp Asp Asn Gly Leu Val Leu Tyr Ser Asn | 500 505 510     |
| 25 | Lys Ala Asn Gly Asn Glu Lys Asn Gly Pro Ile Ile Gln Asn Asn Lys | 515 520 525     |
|    | Phe Glu Tyr Lys Glu Asp Thr Ile Lys Glu Thr Leu Thr Gly Gln Tyr | 530 535 540     |
| 30 | Asp Lys Asn Leu Val Thr Thr Val Glu Glu Glu Tyr Asp Ser Ser Thr | 545 550 555 560 |
|    | Leu Asp Ile Asp Tyr His Thr Ala Ile Asp Gly Gly Gly Tyr Val     | 565 570 575     |
| 35 | Asp Gly Tyr Ile Glu Thr Ile Glu Glu Thr Asp Ser Ser Ala Ile Asp | 580 585 590     |
|    | Ile Asp Tyr His Thr Ala Val Asp Ser Glu Ala Gly His Val Gly Gly | 595 600 605     |
| 40 | Tyr Thr Glu Ser Ser Glu Glu Ser Asn Pro Ile Asp Phe Glu Glu Ser | 610 615 620     |
| 45 | Thr His Glu Asn Ser Lys His His Ala Asp Val Val Glu Tyr Glu Glu | 625 630 635 640 |
|    | Asp Thr Asn Pro Gly Gly Gly Gln Val Thr Thr Glu Ser Asn Leu Val | 645 650 655     |
| 50 | Glu Phe Asp Glu Glu Ser Thr Lys Gly Ile Val Thr Gly Ala Val Ser | 660 665 670     |
|    | Asp His Thr Thr Val Glu Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn | 675 680 685     |
| 55 | Leu Ile Glu Leu Val Asp Glu Leu Pro Glu Glu His Gly Gln Ala Gln | 690 695 700     |



Gly Pro Val Glu Glu Ile Thr Lys Asn Asn His His Ile Ser His Ser  
 705 710 715 720  
 5 Gly Leu Gly Thr Glu Asn Gly His Gly Asn Tyr Asp Val Ile Glu Glu  
 725 730 735  
 Ile Glu Glu Asn Ser His Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu  
 740 745 750  
 10 Gly Gly Gln Asn Ser Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu  
 755 760 765  
 Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Val Asp Ile Asp Phe  
 770 775 780  
 15 Asp Ser Val Pro Gln Ile His Gly Gln Asn Lys Gly Asn Gln Ser Phe  
 785 790 795 800  
 Glu Glu Asp Thr Glu Lys Asp Lys Pro Lys Tyr Glu His Gly Gly Asn  
 805 810 815  
 20 Ile Ile Asp Ile Asp Phe Asp Ser Val Pro His Ile His Gly Phe Asn  
 820 825 830  
 Lys His Thr Glu Ile Ile Glu Glu Asp Thr Asn Lys Asp Lys Pro Ser  
 835 840 845  
 25 Tyr Gln Phe Gly Gly His Asn Ser Val Asp Phe Glu Glu Asp Thr Leu  
 850 855 860  
 Pro Lys Val Ser Gly Gln Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp  
 865 870 875 880  
 30 Thr Thr Pro Pro Ile Val Pro Pro Thr Pro Pro Thr Pro Glu Val Pro  
 885 890 895  
 35 Ser Glu Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu  
 900 905 910  
 Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu  
 915 920 925  
 40 Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ala Glu Pro Gly Lys Pro  
 930 935 940  
 Val Pro Pro Ala Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu  
 945 950 955 960  
 45 Gln Gly Lys Val Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys  
 965 970 975  
 Ala Val Ala Pro Thr Lys Lys Pro Gln Ser Lys Lys Ser Glu Leu Pro  
 980 985 990  
 50 Glu Thr Gly Gly Glu Glu Ser Thr Asn Lys Gly Met Leu Phe Gly Gly  
 995 1000 1005  
 55 Leu Phe Ser Ile Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn  
 1010 1015 1020

His Lys Ala  
1025

(2) INFORMATION FOR SEQ ID NO:5255:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 155 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5255:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Gly | Glu | Lys | Cys | Met | Phe | Leu | Ala | Trp | Asn | Glu | Ile | Arg | Arg | Asn | Lys | 1   | 5   | 10  | 15 |
| Leu | Lys | Phe | Gly | Leu | Ile | Ile | Gly | Val | Leu | Thr | Met | Ile | Ser | Tyr | Leu | 20  | 25  | 30  |    |
| Leu | Phe | Leu | Leu | Ser | Gly | Leu | Ala | Asn | Gly | Leu | Ile | Asn | Met | Asn | Lys | 35  | 40  | 45  |    |
| Glu | Gly | Ile | Asp | Lys | Trp | Gln | Ala | Asp | Ala | Ile | Val | Leu | Asn | Lys | Asp | 50  | 55  | 60  |    |
| Ala | Asn | Gln | Thr | Val | Gln | Gln | Ser | Val | Phe | Asn | Lys | Lys | Asp | Ile | Glu | 65  | 70  | 75  | 80 |
| Asn | Lys | Tyr | Lys | Lys | Gln | Ala | Thr | Leu | Lys | Gln | Thr | Gly | Glu | Ile | Val | 85  | 90  | 95  |    |
| Ser | Asn | Gly | His | Gln | Lys | Asp | Asn | Val | Leu | Val | Phe | Gly | Val | Glu | Lys | 100 | 105 | 110 |    |
| Ser | Ser | Phe | Leu | Val | Pro | Ser | Leu | Ile | Glu | Gly | His | Lys | Ala | Thr | Lys | 115 | 120 | 125 |    |
| Asp | Asn | Glu | Val | Leu | Ala | Asp | Glu | Thr | Leu | Lys | Asn | Lys | Gly | Leu | Lys | 130 | 135 | 140 |    |
| Leu | Gly | Asp | Thr | Leu | Ser | Leu | Ser | Xaa | Xaa | Arg |     |     |     |     |     | 145 | 150 | 155 |    |

Claims

- Computer readable medium having recorded thereon a nucleotide sequence of the *Staphylococcus aureus* genome as depicted in SEQ ID NOS:1-5,191, a representative fragment thereof or a nucleotide sequence at least 95 % identical to a nucleotide sequence depicted in SEQ ID NOS 1-5,191.
- Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a degenerate variant thereof.

3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM) and CD-ROM.
- 5 4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
5. A computer-based system for identifying fragments of the *Staphylococcus aureus* genome of commercial importance comprising the following elements
  - 10 (a) a data storage means comprising the nucleotide sequence of SEQ ID NOS 1-5, 191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS: 1-5, 191;
  - (b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of
  - 15 stop (a) to identify homologous sequence(s), and
  - (c) retrieval means for obtaining said homologous sequence(s) of step (b)
6. A method for identifying commercially important nucleic acid fragments of the *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS: 1-5, 191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS 1-5, 191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.
- 20 7. A method for identifying an expression modulating fragment of *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS 1-5, 191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS: 1-5, 191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.
- 25 8. A protein-encoding nucleic acid fragment of the *Staphylococcus aureus* genome, wherein said fragment comprises the nucleotide sequence of any one of the fragments of SEQ ID NOS 1-5, 191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence, or a degenerate variant of any of the aforementioned sequences.
- 30 9. The nucleic acid fragment of claim 8 which is DNA.
10. The nucleic acid fragment of claim 8 which is RNA.
- 40 11. A vector comprising a fragment of claim 8.
12. A fragment of the *Staphylococcus aureus* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.
- 45 13. A vector comprising a fragment of claim 12.
14. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome of claim 8.
- 50 15. A method for producing a polypeptide in a host cell comprising the steps of
  - (a) incubating an organism of claim 14 under conditions where said fragment is expressed to produce said protein, and
  - 55 (b) isolating said protein
16. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome

of claim 12

17. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 30 to 300 bases 5' to any one of the fragments of the *Staphylococcus aureus* genome depicted in Seq ID Nos 1-5, 191 and Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences
18. A nucleic acid molecule being a homolog of any of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS 1-5, 191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
  - (a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS 1-5, 191 and Tables 2 and 3, including fragments thereof,
  - (b) identifying members of said library which contain sequences that hybridize to said target sequence,
  - (c) isolating the nucleic acid molecules from said members identified in step (b).
19. A DNA molecule being a homolog of any one of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS 1-5, 191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
  - (a) isolating mRNA, DNA, or cDNA produced from an organism,
  - (b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Staphylococcus aureus* genome to prime said amplification,
  - (c) isolating said amplified sequences produced in step (b).
20. A polypeptide encoded by a fragment of claim 8
21. An antibody which selectively binds to any one of the polypeptides of claim 20.
22. A kit for analyzing samples for the presence of polynucleotides derived from *Staphylococcus aureus*, comprising at least one polynucleotide containing a nucleotide sequence of any one of the fragments SEQ ID NOS 1-5, 191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical thereto or a degenerate variant of any of the aforementioned sequences, that will hybridize to a *staphylococcus aureus* polynucleotide under stringent hybridization conditions, and a suitable container.
23. A *Staphylococcus aureus* polypeptide comprising an amino acid sequence identical to an amino acid sequence selected from the group consisting of SEQ ID NOS 5,192 to 5,255 or comprising an amino acid sequence having at least 95% identity to such a sequence.
24. A *Staphylococcus aureus* polypeptide antigen comprising at least one epitope derived from a *Staphylococcus aureus* polypeptide selected from the group consisting of SEQ ID NOS 5,192 to 5,255.
25. A polypeptide comprising at least one epitope encoded by a *Staphylococcus aureus* amino acid sequence selected from the group consisting of the epitopic sequences listed in Table 4
26. The polypeptide of claim 24 or 25, wherein said polypeptide is fixed to a solid phase.
27. A diagnostic kit for detecting *Staphylococcus aureus* infection comprising
  - (a) an isolated polypeptide antigen of claim 24, and
  - (b) means for detecting the binding of an antibody contained in a biological fluid to said antigen
28. A vaccine composition comprising a polypeptide of claim 24 present in a pharmaceutically acceptable carrier
29. A method of vaccinating an individual against *Staphylococcus aureus* infection comprising, administering to an individual the vaccine composition of claim 28.

Figure 1

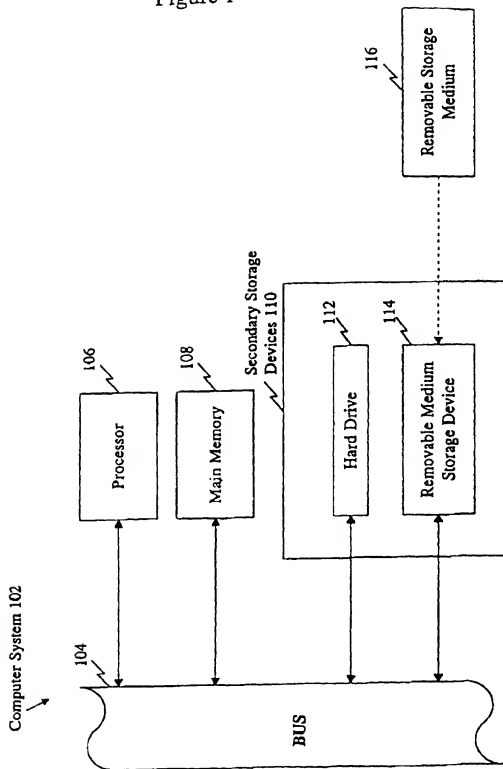


Figure 2

